

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 13:18:09 ; Search time 19 Seconds
(without alignments)
2992.848 Million cell updates/sec

Title: US-10-659-549-3
Perfect score: 3043
Sequence: 1 MALEIHMSDPMCLIEFNFEQ.....GEARSCSQGQVNSQKVVV 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1958.5	64.4	592	A41268	guanine nucleotide
2	1897	62.3	591	S70524	guanine nucleotide
3	1765.5	58.0	589	A46459	macrophage-activat
4	1757.5	57.8	591	S43506	hypothetical prote
5	1365.5	44.9	623	T19684	guanylate binding
6	251.5	8.3	555	T17320	hypothetical prote
7	216	7.1	217	A84810	probable guanylate
8	213.5	7.0	991	H86168	hypothetical prote
9	171.5	5.6	4574	G02520	plectin - human
10	171.5	5.6	4684	A59404	plectin (imported)
11	160.5	5.3	1291	T23382	hypothetical bindin
12	160.5	5.3	1690	T13030	microtubule bindin
13	160.5	5.3	4687	A39638	plectin - rat
14	159.5	5.2	862	T49593	hypothetical prote
15	158	5.2	464	H90279	microtubule bindin
16	156.5	5.1	1410	A57013	early endosome ant
17	155.5	5.1	762	T50155	hypothetical prote
18	154.5	5.1	853	T23697	hypothetical prote
19	154.5	5.1	1392	A43336	microtubule-vesicl
20	154.5	5.1	1427	S22695	restin - human
21	153	5.0	944	S26710	spindle pole body
22	151.5	5.0	992	T46337	hypothetical prote
23	151	5.0	1290	A55094	chromosomal protei
24	151	5.0	1818	S73852	hypothetical prote
25	148	4.9	577	T39804	moesin - pig
26	148	4.9	1288	T46486	chromosomal protei
27	147.5	4.8	429	S23565	apolipoprotein A-I
28	147.5	4.8	1790	S67593	transport protein
29	147	4.8	407	S23325	M2 protein precurs

30	146	4.8	586	1	B41129	ezrin - mouse
31	146	4.8	742	2	S56337	hypothetical prote
32	146	4.8	925	2	T01384	hypothetical prote
33	145.5	4.8	1426	2	T00337	hypothetical prote
34	145	4.8	742	2	C91265	probable vimentin
35	145	4.8	742	2	H86105	probable vimentin
36	145	4.8	1178	2	S78475	mannosylphosphoryl
37	144	4.7	871	2	D86355	protein T18E15.12
38	144	4.7	980	2	E71606	hypothetical prote
39	143.5	4.7	864	2	B90395	purine NTPase [imp
40	143.5	4.7	1875	2	S38173	myosin-like protei
41	143.5	4.7	1992	2	A47297	myosin heavy chain
42	142.5	4.7	1164	2	T24806	hypothetical prote
43	142.5	4.7	2442	2	T08621	centrosome associa
44	142	4.7	657	2	S05517	lamin - chicken
45	142	4.7	1972	1	A41604	myosin heavy chain

ALIGNMENTS

RESULT 1

A41268
guanine nucleotide-binding protein 1 - human
C:Species: Homo sapiens (man)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: A41268
R:Cheng, Y.S.E.; Patterson, C.E.; Staeheli, P.
Mol. Cell. Biol. 11, 4717-4725, 1991
A:Title: Interferon-induced guanylate-binding proteins lack an N(T)KXD consensus motif
A:Reference number: A41268; MUID:91342675; PMID:1715024
A:Accession: A41268
A:Molecule type: mRNA
A:Residues: 1-592 <CHE>
A:Cross-references: UNIPROT:P32455; GB:M55542; NID:g183001; PID:AAA35871.1; PID:g18300
C:Genetics:
A:Gene: GDB:GBPI
A:Cross-references: GDB:378351; OMIM:600411
A:Map position: lpter-lqter
C:Superfamily: guanine nucleotide-binding protein 1

Query Match 64.4%; Score 1958.5; DB 2; Length 592;
Best Local Similarity 69.4%; Pred. No. 7.6e-101;
Matches 387; Conservative 71; Mismatches 89; Indels 11; Gaps 3;

QY	1	MALEIHMSDPMCLIEFNFEQALVQAEILSAITQPVVVVAIVGLYRTGKSYLNNKLAG	60
DB	1	MASEIHMTGPMCLIENTNGRLNANPEALKILSAITQPMVVVAIVGLYRTGKSYLNNKLAG	60
QY	61	KNGGFSVASTVQSHTKGIWICVPHNPWNTLVLDTEGLGDEKADKNNDIQIPALAL	120
DB	61	KKKGFSLSGTVQSHTKGIWICVPHNPWNTLVLDTEGLGDEKADKNNDIQIPALAV	120
QY	121	LLSSFTVNTVNTKIQQAGAILLHNVTETDLKARNSPD-LDRVEDPADSFFPDVLVW	178
DB	121	LLSSFTVNTVNTKIQQAGAILLHNVTETDLKARNSPD-LDRVEDPADSFFPDVLVW	180
QY	179	TURDCLGIEIDQLVTPDEVLNLRPKQSDQVONENLRLCLCIQKFPKKCFIDL	238
DB	181	TURDSLDEADQQLTPDEVLNLRPKQSDQVONENLRLCLCIQKFPKKCFVFR	240
QY	239	PAHOKKLAQLETLPDELEPEFVQVTEFCYSIFGSHMTKTLPGGIVNGSRILNNILVLT	298
DB	241	PVHRKLAQLEKQLDELDPEFVQVADFCYSIFGSHMTKTLPGGIVNGSRILNNILVLT	300
QY	299	VNAISSGDLPCLENVAVLAQRENSAAVQKATAHVDQMQGVQLPMETLQELLDLRYS	358
DB	301	VNAISSGDLPCLENVAVLAQRENSAAVQKATAHVDQMQGVQLPMETLQELLDLRYS	360
QY	359	EREATEVFMKNSFKVDVQSFQKELETLLDAKNDICKRNLEASSDYCSALLKIDFQPLEE	418
DB	361	EREATEVFIIRSFKVDVHDLFQKELAAQLEKKRDKDFCKQNEASSDRCSGLLVIFSPLEE	420


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Qy 301 AISSGDLPCINAVLALAQRENSAAVQAIAYHYDQMGQKVLQPMETIQELLDLHRTSER 360
Db 301 AICSGELPCMENAVLTLLAQIENSAAVQRAITYYEQMNQKIHMPETTLQELLDLHRTCER 360
Qy 361 EAI E V F W K N S F K D V D S F Q K E L T L L D A K Q N D I C K R N L E A S S D Y C A L L K D I F G P L E A V 420
Db 361 E A I E V F W K N S F K D V D Q K F Q E S L G A Q L E A R D A F V K K N D M S S A H C S D L L E G L F A H L E E V 420
Qy 421 K Q G I Y S R P G G H N L F I Q K T E E L K A K Y Y R F R K G I Q A E E V L Q K Y L K S E S V S H A I L O T D Q A L 480
Db 421 K Q G T Y F P G G Y Y L F L R Q K E L E K K Y I Q T P G K L Q A E V M L R K Y F E S K E D L A D T L L K W D Q S L 480
Qy 481 T E T E K K K K A O V K A E A E A E A E A Q R L A A I O R N E Q M Q M E R R L H Q E O V R Q - - - - M E T A K Q N W 536
Db 481 T E K E Q I O E M E R I K A E A E A A N R A L A E M Q K H E M L M E Q K E Q S Y Q E H M K Q L T E K M E Q E R K E L 540
Qy 537 L A E O Q - - - - K W Q E Q Q 547
Db 541 M A E Q O R I I S L K L Q E O E 556

RESULT 4
S43506
hypotheoretical protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S43506
R;Aaundi, V.K.; Stahl, R.C.; Showalter, L.; Conner, K.J.; Carey, D.J.
Biochim. Biophys. Acta 1217, 257-265, 1994
A;Title: Molecular cloning and characterization of an isoprenylated 67 kDa protein
A;Reference number: S43506; MUID:94198287; PMID:8148370
A;Accession: S43506
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-591 <ASU>
A;Cross-references: UNIPROT:Q63663; EMBL:M80367; NID:G207604; PDB:AAA19909.1
C;Superfamily: guanine nucleotide-binding protein 1

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[illegible]

RESULT 6

	Db	395	NQMDLMSNSK KLQQSLSTWNLLKKQJGEBRKNMKY QRYESAI DICK--	448
	Qy	398	LEASDYCSALLKDI FGPLEAVKGYISKPGGNLFIOKTTEUKAKYRYEPRKG OABE	457
	Db	449	--LSDOFKQRINDL-----ESKCKSIHDE---HSNLMVLGSTR-----LEASE	487
	Qy	458	VLOQY--LKSKESVSHAILQTDOALTEPEKKKEAQVKAB-----AEKAEORLAAI QON	511
	Db	488	WKRKYEGTLDNGVSNIRGVDSITRCNSKLI DWIKYENTVSEQKAVTEKIAAMEEK	547
	Qy	512	EQ-----MMQBERLRHQCVROME AKQNLWLAEOQKMQEQOQHVPINCIS	557
	Db	548	KQASTTBEDGLRAEPFRVLDEXEKIIITEKAAK LATLEQLASTRABLKKSAUKV-DECSS	606
	Qy	558	PLPVTMRVCSSGKEGEAARS	577
	Db	607	AKDVRLQMSLLINEKYESVKS	626

RESULT 9
G02520
plectin - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
C;Accession: G02520
R;McLean, W.H.I.; Smith, F.J.D.
submitted to the EMBL Data Library, March 1996
A;Reference number: H01385
A;Accession: G02520
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-4574 <MCL>
A;Cross-references: EMBL:U53204; NID:g1477645; PIDN:AAB05427.1; PID:g1477646
C;Genetics:
A;Gene: PLECL
C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S
F;68-283/Domain: alpha-actinin actin-binding domain homology <ACT>

Db 2556 QLRERQRRQQQME 2569

RESULT 10
A59404
plectin [imported] - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: C59404; A59404
R;Aliu, C.G.; Maercker, C.; Castanon, M.J.; Hauptmann, R.; Wiche, G.
Proc. Natl. Acad. Sci. U.S.A. 93, 4278-4283, 1996
A;Title: Human plectin: organization of the gene, sequence analysis, and chromo-
A;Reference number: C59404; MUID:96210632; PMID:8633055
A;Accession: C59404
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4684 <STO>
A;Cross-references: UNIPROT:Q15149; GB:CAA91196; NID:G1296662; PIDN:CAA91196.1
C;Superfamily: plectin; alpha-actinin actin-binding domain homolog; ribosomal

RESULT 11
T22382
hypothetical protein F48F5.1 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22382
R:Illyod, C.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19558
A:Accession: T22382
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1291 <WIL>
A:Cross-references: UNIPROT:Q9XV10; EMBL:Z81541; PIDN: CAB04411.1; GSPDB:GN0
A:Experimental source: clone F48F5
C:Genetics:

A;Gene: CESP:F48Fs.1
A;Map position: 5
A;Introns: 753/2; 814/3; 987/2; 1030/3; 1114/2; 1153/3; 1222/3

Query Match 5.3%; Score 160.5; DB 2; Length 1291;
Best Local Similarity 18.7%; Pred. No. 0.38;
Matches 143; Conservative 100; Mismatches 224; Indels 299; Gaps 31;

Qy 14 IENFNEQLK-----VNOEALILISAITOPVVVVAIVGLVYRTGSKYLMNKLKAG 60
Db LSRVNEKLKSTFPADNARQVSFQKEESFSVPTDAVSAVGVLAEYKK-----CNHLGG 341

Qy 61 -----KNKGSFVASTVQSHTKGIWICVPHNPENHTLVLL-----DTEGLGDVEKADNK 110
Db 342 PQTDERPGEHFAKVKAS-----VGDSLIALHMFPSQTLALDQLEK----- 382

Qy 111 NDIQIFALAL-----LLSSTFYNTVNVKIDQCA--IDLHNVTETLTLKARNSPDL 160
Db 383 -DVADFVKSLTFTDINNQTLSGEITVKVEDIKKSGKLAKIQENVKSTEDKINGIKLKNL 441

Qy 161 DRVEDPADSASFFPDVLWTLRDFCLGLEIDQLVTPDEYLENSLRPGQSDQRVQNFNLP 220
Db 442 ESTLLPNNSFIQDVMPK-----EVITAETSVSG----- 471

Qy 221 RLCIQKFPKKKCFIDLPAPHKKLAQLETLDPDDELEPEFVQVTEFCYSYFHSM--TK 278
Db 472 --CLQK-LKAKSLVTVQAIATIQKLKL-----DKUL-LESVQQTAKSVSQ-FSETLASVK 522

Qy 279 TLPGGIMVNGSRLKNLVLTYVNAISSGDLPCIEANAVLALAORENSAAVQKAIH- 332
Db 523 KIPDAMKKN-----VKNVTLELNKRSLSNQSDAISHSASALR 560

Qy 333 -----YDQWQGO-----KVQLPME--TLQELLDLHRTS--EREALVEFMK 368
Db 561 SVFGLVKLESSIGQLNDTIVSSEIDKIKIIPAERKMKLQKLWGNHTEGMVSLQAAVQAK 620

Qy 369 NSFQKDVQS-----FOKELETLLDAKO----- 390
Db 621 AFVAKIDVSKLTLNNYSAILKTLETMPDVQWEALEKSEVLEILIRALSAFTERRRRAAG 680

Qy 391 -----NDICKNLEASSDYC-----SALLKDIQFPLBEAVKQGIYS 426
Db 681 SNAHLVAAKVILDKIALDLQFSSNIAHFKNAPLAFQSFSLAKFF-----ATQKISA 735

Qy 427 KPGG-----HNLFI 435
Db 736 SONGGGGGGSGESFPFVIVVWSTVGALLALAAFLAVLYGFHQKQAKIDRDNKEI 795

Qy 436 QKTEELKAKYRPRKGIQABE-VLQKYLKSKESVSHAI-----LQTDQAL 480
Db 796 RDEIEMEARQAEENEQRIAAEKNALEAKIKEKSNWRKVVDEQNQRKDELQAKLRADQEK 855

Qy 481 TETEK-----KKKEAQVKAEBKAEQAQRLAAIQRQNEQNMQRERLHQEQVRQM 529
Db 856 SEARKIAEKKDQEQKEKAKLRADQESKARKVAE--KKKDEQVQKEKDKLQAKLRADQ 914

Qy 530 EIAKQNWLAEOQKMQEQWQVFINCF--ISPLP-VTMVVCSSGKEG 572
Db 915 EKSEARKIAEKKKKEDEAQVKYKNIWGHKKWRFTTLRACADFIEG 960

RESULT 12
Tl3030
microtubule binding protein D-CLIP-190 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: Tl3030
R;Lantz, V.A.; Miller, K.G.
J.;Cell Biol. 140, 897-910, 1998
A;Title: A class VI unconventional myosin is associated with a homologue of a microtubul
A;Reference number: 217588; MUID:98139549; PMID:9472041
A;Accession: Tl3030
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
A;Residues: 1-1690 <LAN>
A;Cross-references: EMBL:AF041382; NID:g2773362; PID:g2773363; PIDN:AAB96783.1
A;Experimental source: strain Oregon R
C;Genetics:
A;Cross-references: FlyBase:FBgn0020503
C;Keywords: cytoskeleton

Query Match 5.3%; Score 160.5; DB 2; Length 1690;
Best Local Similarity 20.8%; Pred. No. 0.54;
Matches 114; Conservative 90; Mismatches 185; Indels 159; Gaps 26;

Qy 104 VEKADNKNDIQIFALALLLSSTFYNTVNVKIDQCAIDL---LHNVTETLTLKARNSPDL 160
Db 385 VERLDREDANQALQL-----QKNINELKARIVLESALGNRKKTEELQC---SI 433

Qy 161 DRVEDPADSASFFPDVLWTLRDFCLGLEIDQLVTPDEYLENSLRPGQSDQRVQNFNLP 220
Db 434 DEAQ-----FC-GDELNAQSQVYKEKIH-----LESKITKLVS 467

Qy 221 RLCIQKFPKKKCFIDLP---AHQKKLAQLE---TLPDDELEPEFVQ---VTEF 267
Db 468 TPSIQSLPP-----DLPSSDDGALQEEIAQLQEKWTIIQKEVESRIAEQLEESQRLREN 521

Qy 268 CSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVNAISSGDLPC-IEN--AVLALAORENSA 324
Db 522 VKYL--NEQIATLQSELVSKDEALEKFSLS-----ECGIENLRRELALLKEENEK 569

Qy 325 AVQKAIHYDQMGQKVQLPMETLQELLDLHRTS---EREAL-----EVFMKN- 369
Db 570 QAQPAQAQEFTRKLAESVEVLRLSSELQNLKATSDLSERSVKNKSDECEILQTEVRMRDE 629

Qy 370 SFKDVQSQFOKELETLLDAKONDICKNLEASSDYCSALLKDIQFPLEEAVKQGIYSKPG 429
Db 630 QIRELNQOLD-EVTTQLNVOKAD-----SSALDDML-----RLQKEGTEEK-- 669

Qy 430 GHNLFIQKTEELKAKYRPRKGIQABEVLQKYLK----- 464
Db 670 --STLLEKTEKELVQIKEQAQAKTLQDKQEQLKQISDLKLAQEBKLVREKTENAINQIQ 727

Qy 465 SKESVSHAILQTDQALQETETEKKKKAEQVKAEBKAE-----AQRLAAIQRQNEQ 513
Db 728 EKESIEQQLALKQNELEDFOKKQSESVHLQEIKAQNTQKDELVELVESGESLKKLQOOLEE 787

Qy 514 MMQERERLHQVRQMEIAQKNWLAEOQKMQE--QOMOVFINCFISPLPVT-----MR 564
Db 788 KTLGHEKL---QAALBELKKEKETIIRKEQEQLQQLQSKSAESESALKVQVQVLEQLQQQ 844

Qy 565 VCSSGKEG 572
Db 845 AAASGSEG 852

RESULT 13
A39638
plectin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A39638; S21876
R;Wiche, G.; Becker, B.; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.; Stratawa
J.;Cell Biol. 114, 83-99, 1991
A;Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide chain with
A;Reference number: A39638; MUID:91268156; PMID:2050743
A;Accession: A39638
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-4687 <WIC>
A;Cross-references: UNIPROT:P30427; EMBL:X59601; NID:g1292885; PIDN:CAA42169.1; PID:g156
C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S
C;Keywords: cytoskeleton; transmembrane protein
P;6-103/Domain: ribosomal protein S10 homology <RS10>
P;184-399/Domain: alpha-actinin actin-binding domain homology <ACT>

Query Match 5.3%; Score 160.5; DB 1; Length 4687;
Best Local Similarity 18.3%; Pred. No. 1.9; Mismatches 135; Indels 13; Gaps 13;
Matches 80; Conservative 79; Mismatches 143; Indels 135; Gaps 13;

QY 190 DQGLVTPDEYLENSLRPKQSDQDQVQNFNRLCLCIQKFPF 229
DB 194 DH-IG-----VTFPLANRLNTLIQDLTHIWSSISKPALENSKIETY----- 233

QY 230 KKKCFIDLPAPAKKLAQLETLPPDELEPEFVQVTEPCSYIFSHMTKTLPGGIMVNGS 289
DB 234 ----PDFAFALPKILQ-----PD-----KFISEVQNL-----GSRFIAGH 266

QY 290 RLKNLVITYNAISSGDLPCINAVLALAAQRENSAAVOKAIAHYDQMGKQVQLPMETLQ 349
DB 267 RNKD-----SDATDDQELTGGVFLP----- 286

QY 350 ELLDLHRTSREAEIEFMKN-----SPKVDQSFQKELETLTLLDAKQNDICKRNLEASSD 403
DB 287 ---BYHRRIPADGLSIYAEGIWQIVSNKOLDLPQOE---LLAQFRCEIAREVQIAFD 340

QY 404 YCSALLKIDIFGLEEAVKQGIYSKPG---GHNLFQKTEELKAKYR---EPRKGIOAE 456
DB 341 AAIAPLEEQQAESTRACKPAVLNQLQIGABAREKCVNFQTSRHHKGVYTKRAELE 400

QY 457 EVLQKYLKS-----KESVSHAILQTDQA-----LTETEKKKKBAQ 491
DB 401 DKIDNRLKALYQAHLTAAHKAGVTAFSEAVANAVKAGKAGGAYEFAIVEKQKTKLEI 460

QY 492 VKAEAEKAEQRLAAIORQNEQMOBRE-----RLHQEQVROMEIAKQNLWLABQKQKOE 545
DB 461 FKKEAQSLAIPGVANWSFKQYLIFEKELDEVSARLKEEMRLAIRVERVKS----- 515

QY 546 QQMQVFNCRISPLPVTMRVCSCKEGEAARSCG-----SQQVMSQKVM 590
DB 516 -----LGDATGLEFNKLIGSGRGSGAPESGKPEATEKDIN-DRVM 554

RESULT 15
H90279
microtubule binding protein, probable [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: H90279
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyaz, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.;
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: H90279
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-464 <KUR>
A:Cross-references: UNIPROT:Q9UXN4; GB:AE006641; NID:G13814451; PIDN:AAK41495.1; GSPDB:G-
C:Genetics:
A:Gene: SS01256

Query Match 5.2%; Score 158; DB 2; Length 464;
Best Local Similarity 23.0%; Pred. No. 0.14;
Matches 85; Conservative 81; Mismatches 136; Indels 68; Gaps 17;

QY 251 LPDDEL-----EPEFVQVTEFCYSYIFSH---SMTKTLPGGIMVNGSRLKNLVTYNAL 302
DB 2 LKDDILKLLKEDAEFRKQVBEILGISFINVTADLKDILKGLLASMKMLKSSVDQLVDAQ 61

QY 303 SSGD--LPCINAV--LALAAQRENSAAVOKAIAHYDQMGKQVQLPMETLQELDLHRTS 358
DB 62 RRAERAKLENVAQVLEAQRKTRDITKL-----EESTKLE---QAVQELIEAQKH 113

QY 359 EREAIEVFMKNKSVKVDQSFQKELETLTLLDAKQNDICKRNLEASSDYCSALLKIDIFGLEE 418
DB 114 DERITK--LSESTKLEQAVQELIEA---QKHDERITKLEESTK-----KLEQ 157

QY 419 AVKQGIYSKGGHNLFTQKTEELKAKYRPERKGIOAEVLOKYLKSKESVSHAILQTDQ 478
DB 158 AVQELIEAQK-KHDERITKLEESTKLEQAVQELIEAQKHDERITKLEESTKLEQAVQ 216

Query Match 5.2%; Score 159.5; DB 2; Length 862;
Best Local Similarity 19.4%; Pred. No. 0.26;
Matches 126; Conservative 102; Mismatches 228; Indels 193; Gaps 27;

QY 14 IENEFQKVNQEALEILSAITQPVV-----VVAIVGLYRTGSKSYLMNKLAKNGKGSVA 68
DB 27 IOVINEDQYNTNLNLYNETHVAEGPNYHLISVFGSQSTGKSTLNLHFGTQ--FSVM 84

QY 69 STVQSH--TKGIWCVPHPNPHNTLVLLDTGEGDVGEKADKNNDIQIFAL--ALLISST 125
DB 85 SERERRQTKGIWMSKKNKMGKADNLIIVMDVEGTDGREGEDQDFERKSFALFALATSEV 144

QY 126 FVYNTVK---IDOGA-IDLHNVTETDLKARNSPDLDRVEDPASPFPDLVTLR 181
DB 145 LIVNIWEHQVGLYQGANNGLLTKTFEVNMQLFLDKQKQNR-----SLUFF-----VIR 193

RESULT 14
T49593
hypothetical protein B3E4.60 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T49593
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022
A:Accession: T49593
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-862 <SCH>
A:Cross-references: UNIPROT:Q9PSX6; EMBL:AL355931; GSPDB:GN00116; NCSP:B3E4.60
A:Experimental source: BAC clone B3E4; strain OR74A
C:Genetics:
A:Gene: NCSP:B3E4.60
A:Map position: 6
A:Introns: 181/2; 764/1
C:Superfamily: Saccharomyces cerevisiae probable membrane protein YOR165w

Query Match 5.2%; Score 159.5; DB 2; Length 862;
Best Local Similarity 19.4%; Pred. No. 0.26;
Matches 126; Conservative 102; Mismatches 228; Indels 193; Gaps 27;

QY 14 IENEFQKVNQEALEILSAITQPVV-----VVAIVGLYRTGSKSYLMNKLAKNGKGSVA 68
DB 27 IOVINEDQYNTNLNLYNETHVAEGPNYHLISVFGSQSTGKSTLNLHFGTQ--FSVM 84

QY 69 STVQSH--TKGIWCVPHPNPHNTLVLLDTGEGDVGEKADKNNDIQIFAL--ALLISST 125
DB 85 SERERRQTKGIWMSKKNKMGKADNLIIVMDVEGTDGREGEDQDFERKSFALFALATSEV 144

QY 126 FVYNTVK---IDOGA-IDLHNVTETDLKARNSPDLDRVEDPASPFPDLVTLR 181
DB 145 LIVNIWEHQVGLYQGANNGLLTKTFEVNMQLFLDKQKQNR-----SLUFF-----VIR 193

Query Match 5.3%; Score 160.5; DB 1; Length 4687;
Best Local Similarity 18.3%; Pred. No. 1.9; Mismatches 135; Indels 13; Gaps 13;
Matches 80; Conservative 79; Mismatches 143; Indels 135; Gaps 13;

QY 190 DQGLVTPDEYLENSLRPKQSDQDQVQNFNRLCLCIQKFPF 229
DB 194 DH-IG-----VTFPLANRLNTLIQDLTHIWSSISKPALENSKIETY----- 233

QY 230 KKKCFIDLPAPAKKLAQLETLPPDELEPEFVQVTEPCSYIFSHMTKTLPGGIMVNGS 289
DB 234 ----PDFAFALPKILQ-----PD-----KFISEVQNL-----GSRFIAGH 266

QY 290 RLKNLVITYNAISSGDLPCINAVLALAAQRENSAAVOKAIAHYDQMGKQVQLPMETLQ 349
DB 267 RNKD-----SDATDDQELTGGVFLP----- 286

QY 350 ELLDLHRTSREAEIEFMKN-----SPKVDQSFQKELETLTLLDAKQNDICKRNLEASSD 403
DB 287 ---BYHRRIPADGLSIYAEGIWQIVSNKOLDLPQOE---LLAQFRCEIAREVQIAFD 340

QY 404 YCSALLKIDIFGLEEAVKQGIYSKPG---GHNLFQKTEELKAKYR---EPRKGIOAE 456
DB 341 AAIAPLEEQQAESTRACKPAVLNQLQIGABAREKCVNFQTSRHHKGVYTKRAELE 400

QY 457 EVLQKYLKS-----KESVSHAILQTDQA-----LTETEKKKKBAQ 491
DB 401 DKIDNRLKALYQAHLTAAHKAGVTAFSEAVANAVKAGKAGGAYEFAIVEKQKTKLEI 460

QY 492 VKAEAEKAEQRLAAIORQNEQMOBRE-----RLHQEQVROMEIAKQNLWLABQKQKOE 545
DB 461 FKKEAQSLAIPGVANWSFKQYLIFEKELDEVSARLKEEMRLAIRVERVKS----- 515

QY 546 QQMQVFNCRISPLPVTMRVCSCKEGEAARSCG-----SQQVMSQKVM 590
DB 516 -----LGDATGLEFNKLIGSGRGSGAPESGKPEATEKDIN-DRVM 554

RESULT 15
H90279
microtubule binding protein, probable [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: H90279
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyaz, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.;
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: H90279
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-464 <KUR>
A:Cross-references: UNIPROT:Q9UXN4; GB:AE006641; NID:G13814451; PIDN:AAK41495.1; GSPDB:G-
C:Genetics:
A:Gene: SS01256

Query Match 5.2%; Score 158; DB 2; Length 464;
Best Local Similarity 23.0%; Pred. No. 0.14;
Matches 85; Conservative 81; Mismatches 136; Indels 68; Gaps 17;

QY 251 LPDDEL-----EPEFVQVTEFCYSYIFSH---SMTKTLPGGIMVNGSRLKNLVTYNAL 302
DB 2 LKDDILKLLKEDAEFRKQVBEILGISFINVTADLKDILKGLLASMKMLKSSVDQLVDAQ 61

QY 303 SSGD--LPCINAV--LALAAQRENSAAVOKAIAHYDQMGKQVQLPMETLQELDLHRTS 358
DB 62 RRAERAKLENVAQVLEAQRKTRDITKL-----EESTKLE---QAVQELIEAQKH 113

QY 359 EREAIEVFMKNKSVKVDQSFQKELETLTLLDAKQNDICKRNLEASSDYCSALLKIDIFGLEE 418
DB 114 DERITK--LSESTKLEQAVQELIEA---QKHDERITKLEESTK-----KLEQ 157

QY 419 AVKQGIYSKGGHNLFTQKTEELKAKYRPERKGIOAEVLOKYLKSKESVSHAILQTDQ 478
DB 158 AVQELIEAQK-KHDERITKLEESTKLEQAVQELIEAQKHDERITKLEESTKLEQAVQ 216

Query Match 5.2%; Score 159.5; DB 2; Length 862;
Best Local Similarity 19.4%; Pred. No. 0.26;
Matches 126; Conservative 102; Mismatches 228; Indels 193; Gaps 27;

QY 14 IENEFQKVNQEALEILSAITQPVV-----VVAIVGLYRTGSKSYLMNKLAKNGKGSVA 68
DB 27 IOVINEDQYNTNLNLYNETHVAEGPNYHLISVFGSQSTGKSTLNLHFGTQ--FSVM 84

QY 69 STVQSH--TKGIWCVPHPNPHNTLVLLDTGEGDVGEKADKNNDIQIFAL--ALLISST 125
DB 85 SERERRQTKGIWMSKKNKMGKADNLIIVMDVEGTDGREGEDQDFERKSFALFALATSEV 144

QY 126 FVYNTVK---IDOGA-IDLHNVTETDLKARNSPDLDRVEDPASPFPDLVTLR 181
DB 145 LIVNIWEHQVGLYQGANNGLLTKTFEVNMQLFLDKQKQNR-----SLUFF-----VIR 193

Qy	479	ALTETKKE-----AQVKAEEAEQRLAAIQORONEQMMOERERLHQ	523
Db	217	ELIEAQKHDERITKLESTKLEQAVQELIEAQKHDERITKLE-ESIQLYDAQRAE	275
Qy	524	EQVRQMEIAKQNWLAEOQKQEQQVFINCISPL-PVTMRVCS--GKEG---EAARS	577
Db	276	ERIAKLENAVEQ-LVEAQKRTDER-----ITKLEEVTKLVESQLGMQNEIRELRKA	326
Qy	578	CGSOQGVWSQ	587
Db	327	LGSNGKRWGR	336

Search completed: July 9, 2005, 13:25:47
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 13:19:44 ; Search time 43 Seconds
(without alignments)
1025.991 Million cell updates/sec

Title: US-10-659-549-3

Perfect score: 3043
Sequence: 1 MALEIHMSDPCLIEFNFEQ.....GEAARSCGQGVWSQKVV 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3043	100.0	591	4	US-09-643-657-3
2	2610.5	85.8	633	2	US-08-736-770-3
3	1966.5	64.6	605	4	US-09-949-016-8823
4	1958.5	64.4	592	2	US-08-736-770-6
5	1958.5	64.4	592	4	US-09-702-705-1809
6	1958.5	64.4	592	4	US-09-736-457-1809
7	1958.5	64.4	592	4	US-09-643-657-4
8	1958.5	64.4	592	4	US-09-671-325-1809
9	1897	62.3	591	2	US-08-736-770-5
10	1897	62.3	591	4	US-09-643-657-5
11	1881	61.8	608	2	US-08-736-770-1
12	1832.5	60.2	583	4	US-09-949-016-8267
13	1765.5	58.0	589	4	US-09-643-657-14
14	1757.5	57.8	591	4	US-09-643-657-15
15	1459.5	48.0	620	4	US-09-643-657-13
16	932.5	30.6	573	4	US-09-643-657-18
17	526	17.3	147	4	US-09-370-838-99
18	526	17.3	147	4	US-09-854-133-99
19	509	16.7	159	4	US-09-370-838-98
20	509	16.7	159	4	US-08-854-133-98
21	392	12.9	96	4	US-09-513-999C-5037
22	296	9.7	103	4	US-09-643-657-16
23	239	7.9	67	4	US-09-643-657-17
24	203	6.7	57	4	US-09-621-976-4483
25	197	6.5	573	4	US-09-270-767-44491
26	154.5	5.1	1427	4	US-09-538-092-1044
27	151	5.0	1180	4	US-09-543-681A-6436

Sequence 5067, Ap
Sequence 209, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 10580, A
Sequence 91, Appl
Sequence 1084, Ap
Sequence 7111, Ap
Sequence 7112, Ap
Sequence 7113, Ap
Sequence 4, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 7037, Ap
Sequence 7646, Ap

28 148 4.9 710 4 US-09-107-532A-5067
29 148 4.9 1288 4 US-09-919-039-209
30 146.5 4.8 1531 4 US-09-418-710-29
31 146.5 4.8 1531 4 US-09-839-479-29
32 145.5 4.8 568 4 US-09-949-016-10580
33 144 4.7 1857 4 US-09-917-254-91
34 144 4.7 1972 4 US-09-538-092-1084
35 144 4.7 1984 4 US-09-949-016-7111
36 144 4.7 1984 4 US-09-949-016-7112
37 144 4.7 1984 4 US-09-949-016-7113
38 142 4.7 1972 4 US-08-875-435B-4
39 141.5 4.7 1527 4 US-09-418-710-27
40 141.5 4.7 1527 4 US-09-839-479-27
41 140.5 4.6 897 1 US-08-095-737-4
42 140.5 4.6 897 1 US-08-480-145-4
43 140.5 4.6 897 2 US-08-477-389-4
44 140.5 4.6 1540 4 US-09-949-016-7037
45 140.5 4.6 2107 4 US-09-949-016-7646

ALIGNMENTS

RESULT 1
US-09-643-657-3
; Sequence 3, Application US/09643657
; Patent No. 6642024
; GENERAL INFORMATION:
; APPLICANT: Diane Pennica
; TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,657
; FILING DATE: 17-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,089A
; FILING DATE: 29-Jan-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1056
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-643-657-3

Query Match 100.0%; Score 3043; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.7e-254;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MALEIHMSDPCLIEFNFEQKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKL 60
Db 1 MALEIHMSDPCLIEFNFEQKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKL 60

Qy 61 KNKGFSVASTVQSHTKGIWICVPHNPWNTLVLDTDEGLGDVEKADNKNNDIQIFALAL 120
Db 61 KNKGFSVASTVQSHTKGIWICVPHNPWNTLVLDTDEGLGDVEKADNKNNDIQIFALAL 120
Qy 121 LLSSTFYVNTVNTKIDQGAIDLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
Db 121 LLSSTFYVNTVNTKIDQGAIDLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
Qy 181 RDCFLGLEIDQVLTDPDEYLENSLRPKQSGDQVONFNLPRLCIOKFFPKKCFIFDLP 240
Db 181 RDCFLGLEIDQVLTDPDEYLENSLRPKQSGDQVONFNLPRLCIOKFFPKKCFIFDLP 240
Qy 241 HQKLAQLETLDPDELEPEFVQVTEFCYSYIFSHSMTKTLPGGIMVNGSRLLKNLVLTYV 300
Db 241 HQKLAQLETLDPDELEPEFVQVTEFCYSYIFSHSMTKTLPGGIMVNGSRLLKNLVLTYV 300
Qy 301 AISSGDLPCINAVLALAQRENSAAVQKAIHAYDQMGQKQVLPMTLOELLDLHRTSER 360
Db 301 AISSGDLPCINAVLALAQRENSAAVQKAIHAYDQMGQKQVLPMTLOELLDLHRTSER 360
Qy 361 EAIEVFWMKNSFKVDQSFQKELETLDDAKONDICKRNLEASSDYCSALLKDIIFGPLEAV 420
Db 361 EAIEVFWMKNSFKVDQSFQKELETLDDAKONDICKRNLEASSDYCSALLKDIIFGPLEAV 420
Qy 421 KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480
Db 421 KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480
Qy 481 TETEKKKKEAQVKAEEAKAEQAORLAAIORQNEQMMQERERLHQBQVQMEIAKQNWLAEQ 540
Db 481 TETEKKKKEAQVKAEEAKAEQAORLAAIORQNEQMMQERERLHQBQVQMEIAKQNWLAEQ 540
Qy 541 QKMQEQQOMQVFINCFISPLPVTMVCSSGKEGEAARSCGSGQGVMSOKVMV 591
Db 541 QKMQEQQOMQVFINCFISPLPVTMVCSSGKEGEAARSCGSGQGVMSOKVMV 591

RESULT 2

US-08-736-770-3
; Sequence 3, Application US/08736770
; Patent No. 5871965
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN GUANYLATE BINDING PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/736,770
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0145 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 633 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
; US-08-736-770-3

Query Match 85.8%; Score 2610.5; DB 2; Length 633;
Best Local Similarity 94.4%; Pred. No. 4.8e-217;
Matches 519; Conservative 8; Mismatches 20; Indels 3; Gaps 3;

Qy 1 MALEIHMSDPMCIENFNEQKVNQEALETLSAITQPVVVVAIVGLVYRTKSYLMNKLKAG 60
Db 1 MALEIHMSDPMCIENFNEQKVNQEALETLSAITQPVVVVAIVGLVYRTKSYLMNKLKAG 60
Qy 61 KNKGFSVASTVQSHTKGIWICVPHNPWNTLVLDTDEGLGDVEKADNKNNDIQIFALAL 120
Db 61 KNKGFSVASTVQSHTKGIWICVPHNPWNTLVLDTDEGLGDVEKADNKNNDIQIFALAL 120
Qy 121 LLSSTFYVNTVNTKIDQGAIDLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
Db 121 LLSSTFYVNTVNTKIDQGAIDLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
Qy 181 RDCFLGLEIDQVLTDPDEYLENSLRPKQSGDQVONFNLPRLCIOKFFPKKCFIFDLP 239
Db 179 KDFCLGLEIDQVLTDPDEYLENSLRPKQSGDQVONFNLTPSVVYRSSFOKKWFIKFLP 238
Qy 240 AHQKLAQLETLDPDELEPEFVQVTEFCYSYIFSHSMTKTLPGGIMVNGSRLLKNLVLTYV 299
Db 239 AHQKLAQLETLDPDELEPEFVQVTEFCYSYIFSHSMTKTLPGGIMVNGSRLLKNLVLTYV 298
Qy 300 NAISSGDLPCINAVLALAQRENSAAVQKAIHAYDQMGQKQVLPMTLOELLDLHRTSE 359
Db 299 NAISSGDLPCINAVLALAQRENSAAVQKAIHAYDQMGQKQVLPMTLOELLDLHRTSE 358
Qy 360 REAIEVFWMKNSFKVDQSFQKELETLDDAKONDICKRNLEASSDYCSALLKDIIFGPLEEA 419
Db 359 REAIEVFWMKNSFKVDQSFQKELETLDDAKONDICKRNLEASSDYCSALLKDIIFGPLEEA 418
Qy 420 VKQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQ 479
Db 419 VKQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQ 478
Qy 480 LTETEKKKKEAQVKAEEAKAEQAORLAAIORQNEQMMQERERLHQBQVQMEIAKQNWLA 539
Db 479 LTETEKKKKEAQVKAEEAKAEQAORLAAIORQNEQMMQERERLHQBQVQMEIAKQNWLA 538
Qy 540 QKMQEQQOMQ 549
Db 539 QKMQEQQOMQ 548

RESULT 3

US-09-949-016-8823
; Sequence 8823, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08

QY	121	LLSSTFVNTVNTKIDQGAIDLLHNVTETDLLKARNSPDLRVEDPADSASFFPDLVWTL	180	PR	07-OCT-1998;	98WO-US021141.
Db	121			PR	29-OCT-1998;	98WO-US022991.
QY	181	RDFCGLGIDQVTPDEYLENSLRPKQSDQORVQNFNLPRLCIQKFFPKKCFIFDLPA	240	PR	29-OCT-1998;	98WO-US022992.
Db	181			PR	20-NOV-1998;	98WO-US024855.
QY	241	HOKKLAQLETPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLTVYN	300	PR	01-DEC-1998;	98WO-US025108.
Db	241			PR	05-JAN-1999;	99WO-US000106.
QY	301	AISSGDLFCIENAVLALAQRENSAAVQAIHAYDOQMGQKQVQLPMETLQELLDLHRTSER	360	PR	08-MAR-1999;	99WO-US005028.
Db	301			PR	10-MAR-1999;	99WO-US005190.
QY	361	EAIEVFMKNSFKVDQSFQKLETLDDAKQNDICKRNLKESVSHAILQTDQAL	420	PR	20-APR-1999;	99WO-US008615.
Db	361			PR	14-MAY-1999;	99WO-US010733.
QY	421	KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVQLKYLKSKESVSHAILQTDQAL	480	PR	02-JUN-1999;	99WO-US012252.
Db	421			PR	01-SEP-1999;	99WO-US020111.
QY	481	TETETKKKEAQAQAEAEQAQRLAAIQORQEQMMQERLHQEQVROMETAKQNWLAEQ	540	PR	08-SEP-1999;	99WO-US020594.
Db	481			PR	15-SEP-1999;	99WO-US021090.
QY	541	QKMQEQQMQ 549		PR	15-SEP-1999;	99WO-US021547.
Db	541			PR	05-OCT-1999;	99WO-US023089.
RESULT 4				PR	29-NOV-1999;	99WO-US028214.
ID	ABO17638	standard; protein; 586 AA.		PR	30-NOV-1999;	99WO-US028313.
AC	ABO17638;			PR	01-DEC-1999;	99WO-US028301.
XX	26-AUG-2003	(first entry)		PR	01-DEC-1999;	99WO-US028634.
DE	Novel human secreted and transmembrane protein PRO4987.			PR	02-DEC-1999;	99WO-US028551.
KW	Human; secreted and transmembrane protein; PRO; antiinflammatory;			PR	02-DEC-1999;	99WO-US028564.
KW	antiarteriosclerotic; bardant; anti-infertility; anti-HIV; cytostatic;			PR	16-DEC-1999;	99WO-US030095.
KW	antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;			PR	20-DEC-1999;	99WO-US030911.
KW	TNF-alpha release; cell proliferation; cell differentiation;			PR	20-DEC-1999;	99WO-US030999.
KW	gene expression modulator; proteoglycan release; cytokine release;			PR	22-DEC-1999;	99WO-US030720.
KW	tumour; inflammatory disease; organ failure; atherosclerosis;			PR	30-DEC-1999;	99WO-US031243.
KW	cardiac injury; infertility; birth defect; premature aging; AIDS;			PR	05-JAN-2000;	2000WO-US000219.
KW	acquired immunodeficiency syndrome; cancer; diabetic complication;			PR	06-JAN-2000;	2000WO-US000277.
KW	bioreactor; tissue typing.			PR	11-FEB-2000;	2000WO-US000376.
OS	Homo sapiens.			PR	18-FEB-2000;	2000WO-US004341.
XX	US2003032156-A1.			PR	18-FEB-2000;	2000WO-US004342.
PD	13-FEB-2003.			PR	24-FEB-2000;	2000WO-US004914.
PF	06-MAY-2002; 2002US-00140474.			PR	24-FEB-2000;	2000WO-US005004.
XX	31-MAR-1997; 97WO-US005230.			PR	01-MAR-2000;	2000WO-US005501.
PR	12-JUN-1998; 98WO-US012456.			PR	02-MAR-2000;	2000WO-US005746.
PR	14-JUL-1998; 98WO-US014552.			PR	02-MAR-2000;	2000WO-US005841.
PR	28-AUG-1998; 98WO-US017888.			PR	10-MAR-2000;	2000WO-US006319.
PR	10-SEP-1998; 98WO-US018824.			PR	15-MAR-2000;	2000WO-US006884.
PR	14-SEP-1998; 98WO-US019093.			PR	21-MAR-2000;	2000WO-US007377.
PR	14-SEP-1998; 98WO-US019094.			PR	30-MAR-2000;	2000WO-US007532.
PR	14-SEP-1998; 98WO-US019177.			PR	17-MAY-2000;	2000WO-US008439.
PR	16-SEP-1998; 98WO-US019330.			PR	30-MAY-2000;	2000WO-US013705.
PR	17-SEP-1998; 98WO-US019437.			PR	02-JUN-2000;	2000WO-US014042.
				PR	02-JUN-2000;	2000WO-US014941.
				PR	28-JUN-2000;	2000WO-US015264.
				PR	11-AUG-2000;	2000WO-US020710.
				PR	23-AUG-2000;	2000WO-US022031.
				PR	24-AUG-2000;	2000WO-US023522.
				PR	08-NOV-2000;	2000WO-US030952.
				PR	10-NOV-2000;	2000WO-US030873.
				PR	01-DEC-2000;	2000WO-US032878.
				PR	20-DEC-2000;	2000US-00747259.
				PR	20-DEC-2000;	2000WO-US034956.
				PR	28-FEB-2001;	2001US-00796498.
				PR	28-FEB-2001;	2001WO-US006520.
				PR	01-MAR-2001;	2001WO-US006666.
				PR	09-MAR-2001;	2001US-00802706.
				PR	14-MAR-2001;	2001US-00808689.
				PR	22-MAR-2001;	2001US-00816744.
				PR	05-APR-2001;	2001US-00828366.
				PR	10-MAY-2001;	2001US-00854208.
				PR	10-MAY-2001;	2001US-00854280.
				PR	18-MAY-2001;	2001US-00860216.
				PR	25-MAY-2001;	2001US-00866028.
				PR	25-MAY-2001;	2001US-00866034.

10 Apr 29 11

PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001US-00801116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-347380/32.
 DR N-PSDB; ACD23875.
 XX

XX New secreted and transmembrane PRO nucleic acids, for treating
 PT inflammation, organ failure, atherosclerosis, cardiac injury,
 PT infertility, birth defects, premature aging, acquired immunodeficiency
 PT syndrome (AIDS), or cancer.
 XX

XX Claim 12; Fig 46; 660pp; English.

XX The invention describes an isolated nucleic acid (1) comprising, or which
 CC has 80 % sequence identity to, or the full-length coding sequence of, one
 CC of 275 nucleotide sequences, and which encodes a corresponding
 CC polypeptide selected from 275 amino acid sequences, where all sequences
 CC are given in the specification. The polypeptide encoded by (1) is used to
 CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
 CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
 CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
 CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
 CC the proliferation or differentiation of cells or gene expression, or
 CC stimulate the release of proteoglycans, stimulate the release of cytokine
 CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
 CC to factor VITA, or detect the presence of tumour in a mammal. The nucleic
 CC acid and polypeptide encoded by it, are useful for treating inflammatory
 CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
 CC birth defects, premature aging, acquired immunodeficiency syndrome
 CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
 CC hybridisation probes, in chromosome and gene mapping, and in generating
 CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
 CC This is the amino acid sequence of a novel human secreted and
 CC transmembrane PRO polypeptide

XX Sequence 586 AA;

Query Match 92.5%; Score 2815; DB 6; Length 586;
 Best Local Similarity 100.0%; Pred. No. 1.2e-222;
 Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MALEIHMDDPCLNENFNEQKLVNQEALEILSAITQPVVVAIVGLYRTGKSLMKNLAG 60
 Db 1 MALEIHMDDPCLNENFNEQKLVNQEALEILSAITQPVVVAIVGLYRTGKSLMKNLAG 60
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 Db 61 KNGKFSVASTVQSHTKGIWICVPHNPNTLLDTEGLGDVEKADNKNDIQIFALAL 120
 Qy 121 LLSSTFVYNTVNTKIDQGAIDLLHNVTETLLKARNSPDLRVEDPDADSAFFPDVWTL 180
 Db 121 LLSSTFVYNTVNTKIDQGAIDLLHNVTETLLKARNSPDLRVEDPDADSAFFPDVWTL 180

Qy 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQVRQNFNLPRLCIQKFFPKKCFIPDLPA 240
 Db 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQVRQNFNLPRLCIQKFFPKKCFIPDLPA 240
 Qy 241 HOKKLAQLETLPPDELEPEFVQVTEFCYSIFSHSMTKTLPGGIMVNGSRLKNLVLYYN 300
 Db 241 HOKKLAQLETLPPDELEPEFVQVTEFCYSIFSHSMTKTLPGGIMVNGSRLKNLVLYYN 300
 Qy 301 AISSGDLPCIEANVLALAQRENSAAVQKAIHYDQMGQKQVQLPMETLQELLDLHRTSER 360
 Db 301 AISSGDLPCIEANVLALAQRENSAAVQKAIHYDQMGQKQVQLPMETLQELLDLHRTSER 360
 Qy 361 EAIIEVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKLEASDYCSALLKDIIFGPLEEAV 420
 Db 361 EAIIEVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKLEASDYCSALLKDIIFGPLEEAV 420
 Qy 421 KOGIYSKGGHNLFIQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
 Db 421 KOGIYSKGGHNLFIQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
 Qy 481 TETEKKKKEAQVKAEEAKAEQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAQ 540
 Db 481 TETEKKKKEAQVKAEEAKAEQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAQ 540
 Qy 541 QRMQEQQMQ 549
 Db 541 QRMQEQQMQ 549
 RESULT 5
 ABUS0892
 ID ABUS0892 standard; protein; 586 AA.
 XX
 AC ABUS0892;
 XX
 DT 23-JUN-2003 (first entry)
 XX
 DE Human PRO polypeptide #23.
 XX
 KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;
 KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
 KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
 KW hearing loss; coagulation disorder; stroke; heart attack; cardiac;
 KW antidiabetic; anorectic; vulnery; antiarthritic; osteopathic;
 KW antirheumatic; auditory; cerebroprotective; angiogenic.
 XX
 OS Homo sapiens.
 XX
 XX US2003004311-A1.
 XX
 XX 02-JAN-2003.
 XX
 XX 19-DEC-2001; 2001US-00028072.
 XX
 XX 18-JUN-1997; 97US-0049911P.
 XX 26-AUG-1997; 97US-0056974P.
 XX 17-SEP-1997; 97US-0059113P.
 XX 17-SEP-1997; 97US-0059115P.
 XX 17-SEP-1997; 97US-0059117P.
 XX 17-SEP-1997; 97US-0059122P.
 XX 17-SEP-1997; 97US-0059184P.
 XX 18-SEP-1997; 97US-0059263P.
 XX 19-SEP-1997; 97US-0059352P.
 XX 19-SEP-1997; 97US-0059588P.
 XX 24-SEP-1997; 97US-0059836P.
 XX 17-OCT-1997; 97US-0062250P.
 XX 17-OCT-1997; 97US-0062285P.
 XX 17-OCT-1997; 97US-0062287P.
 XX 17-OCT-1997; 97US-0063755P.
 XX 24-OCT-1997; 97US-0062814P.
 XX 24-OCT-1997; 97US-0062816P.

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PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063082P.
PR 24-OCT-1997; 97US-0063127P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063350P.
PR 28-OCT-1997; 97US-0063561P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063733P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
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PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 11-DEC-1997; 97US-0069212P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 16-DEC-1997; 97US-0069694P.
PR 23-JAN-1998; 98US-0072320P.
PR 04-FEB-1998; 98US-0073612P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 12-MAR-1998; 98US-0077791P.
PR 20-MAR-1998; 98US-0078910P.
PR 25-MAR-1998; 98US-0079294P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079728P.
PR 31-MAR-1998; 98US-0080165P.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 16-DEC-1999; 99WO-US030095.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 01-MAR-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
XX (GETH ) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-352836/33.
XX N-PSDB; ACA67016.
XX New isolated PRO polypeptide useful for treating diabetes, rheumatoid
XX arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
XX heart attack.
XX Claim 12; Fig 46; 643pp; English.
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
XX polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides and polynucleotides are useful for preparing a medicament
XX useful in the treatment of diabetes, bone and/or cartilage disorders
XX (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
XX hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
XX (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
XX assays for PRO, by detecting its expression in specific cells, tissues or
XX serum, and for affinity purification of PRO from recombinant cell culture
XX or natural sources. ABUS0870-ABUS1144 represent the human PRO
XX polypeptides of the invention. Note: The sequence data for this patent
XX was obtained in electronic format directly from the USPTO web site at
XX seqdata.uspto.gov/paipsDIDentry.html
XX Sequence 586 AA;
Query Match 92.5%; Score 2815; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MALEIHMSDPMCLIENTNEQKVNQEALEILSAITQPVVVVAIVGLVTRTGSYLMNKLGA 60
Db 1 MALEIHMSDPMCLIENTNEQKVNQEALEILSAITQPVVVVAIVGLVTRTGSYLMNKLGA 60
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Db 61 KNGGFSVASTVQSHTKGIWICVPHNPNTLVLLDTEGLGDVEKADNKNDIOIFALAL 120
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Db 121 LLSSTFVYNTVKNIDQGAIDLHNVNTELTDLKARNSPDLDRVEDPADSASFFPDVWTL 180
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Db 241 HOKKLAQLETLPPDDELEPEFVQVTEFCSYIFSSHMTKTLPGGIWNGSRKLNVLTVYN 300
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Db 301 AISSGDLPCIEENAVIALAQRENSAAVQKAIYAHYDQMGQKQVQLPMETIQELLDLHRTSER 360
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Db 361 EATIEVFMKNSPKVDQSFQKELETLDDAKNDICKRNLKNEASSDYCSALLKDIQFGLP 420
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PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US004343.
 PR 24-FEB-2000; 2000WO-US004344.
 PR 24-FEB-2000; 2000WO-US004345.
 PR 01-MAR-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005005.
 PR 02-MAR-2000; 2000WO-US005006.
 PR 02-MAR-2000; 2000WO-US005007.
 PR 10-MAR-2000; 2000WO-US005008.
 PR 10-MAR-2000; 2000WO-US005009.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-148238/14.
 DR N-PSDB; ABX89163.
 XX Two hundred and seventy five nucleic acids encoding PRO polypeptides,
 PT useful for treating pericyte-associated tumors, diabetes and various bone
 PT and/or cartilage disorders, e.g. arthritis.
 XX Claim 12; Fig 46; 659pp; English.
 XX The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and

CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumors. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO828, PRO1068 or PRO1132 enhance survival of
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with,
 CC decreased mesangial cell function such as Berger disease or other
 CC nephropathies associated with dermatitis, herpetiformis or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and are
 CC thus useful for treating sports injuries, and arthritis. This is the
 CC amino acid sequence of a novel human PRO protein
 XX
 SQ Sequence 586 AA;

Query Match 92.5%; Score 2815; DB 6; Length 586;
 Best Local Similarity 100.0%; Pred. No. 1.2e-222; Indels 0; Gaps 0;
 Matches 549; Conservative 0; Mismatches 0;

QY 1 MALEIHMSDPMCLIEFNEQKVNQEALEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
 DB 1 MALEIHMSDPMCLIEFNEQKVNQEALEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
 QY 61 KNKGFSVASTVQSHTKGIWCVPHNPNTLLDTEGLGDEVEKADNKNDIQIFALAL 120
 DB 61 KNKGFSVASTVQSHTKGIWCVPHNPNTLLDTEGLGDEVEKADNKNDIQIFALAL 120
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 DB 121 LLSSTFVYNTVTKIDQGAIDLHNVTETLLKARNSPDLDRVEDPADSFFPDVMTL 180
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 DB 181 RDFCLGLEIDQVTPDEYLENSLRPKQSGDQVQNFNLRLCQKFPKKCFIDLPA 240
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 DB 241 HOKKLAQLETLPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLTVN 300
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 DB 301 AISSGDLPCIEENAVLALAORENSAAVKAIHYDQMGQKQVQLPMETLQELDLHRTSER 360
 QY 361 EAEVFMKNSFKVDQSFQKELETLLDAKNDICRNLKNSDYCSALLKDIIFGLEAV 420
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 DB 421 KOGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVLYQKYLKSKESVSHAILQTDQAL 480
 QY 481 TETEKKKAEQVKAEEAKAEQRLAAIQRONEQMQERLHQEVQVROMETAKQNWLAEQ 540
 DB 481 TETEKKKAEQVKAEEAKAEQRLAAIQRONEQMQERLHQEVQVROMETAKQNWLAEQ 540
 QY 541 QKMOEQQMQ 549
 DB 541 QKMOEQQMQ 549

RESULT 8
ABO24863
ID ABO24863 standard; protein; 586 AA.
XX AC ABO24863;
XX DT
XX OS 05-SEP-2003 (first entry)
XX DE Human secreted/transmembrane protein (PRO) #23.
XX KW Human; PRO; secreted protein; transmembrane protein; tumour; cytostatic;
KW gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood;
KW proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell;
KW PBWC; glucose uptake; FFA; skeletal muscle cell; adipocyte cell;
KW chondrocyte cell proliferation; chondrocyte cell differentiation;
KW pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell;
KW endothelial cell; A-peptide; factor VIIA.
XX OS Homo sapiens.
XX PN US2003036179-A1.
XX PD 20-FEB-2003.
XX PF 10-MAY-2002; 2002US-00142431.
XX PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019033.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005801.
PR 02-MAR-2000; 2000WO-US005746.
PR 10-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006319.
PR 20-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032878.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
PA (GETH) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-466355/44.
DR N-PSDB; ACD41817.
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or
PT PRO4978, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX Claim 12; Fig 46; 659pp; English.
XX The invention relates to an isolated nucleic acid comprising at least 80%
CC sequence identity to a PRO (secreted and transmembrane protein) cDNA
CC comprising a nucleic acid (a) encoding a PRO polypeptide, or its
CC extracellular domain (with or without its associated signal peptide),

CC which comprises any of the 275 120-850 residue amino acid sequences,
CC given in the specification; (b) comprising any of the 275 300-3500
CC nucleotide sequences, given in the specification; or (c) comprising the
CC full-length coding sequence of the nucleotide sequences given in the
CC specification, or of the DNA deposited under any of the American Type
CC Culture Collection (ATCC) Accession Numbers listed in the specification.
CC Also included are a vector comprising the novel nucleic acid, a host cell
CC comprising the vector, producing a PRO polypeptide, the isolated PRO
CC polypeptides detailed above, a chimeric molecule comprising the PRO
CC polypeptide of fused to a heterologous amino acid sequence, an anti-PRO
CC antibody, detecting a PRO polypeptide in a sample suspected of containing
CC the PRO polypeptide, linking a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulating at least one biological activity of a cell
CC expressing a PRO polypeptide, stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, (or proteoglycans from
CC cartilage or cytokine from peripheral blood mononuclear cells (PBMC)),
CC modulating the uptake of glucose or FFA by skeletal muscle cells or
CC adipocyte cells, stimulating the proliferation or differentiation of
CC chondrocyte cells (or proliferation of or gene expression in pericyte
CC cells), stimulating the proliferation of inner ear utricular supporting
CC cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the
CC binding of A-peptide to factor VIIA, or differentiation of adipocyte
CC cells, detecting the presence of a tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences given
CC in the specification. The polynucleotide is useful in molecular biology,
CC including uses as hybridisation probes, in chromosome and gene mapping,
CC in generating antisense RNA and DNA, and in gene therapy. The
CC polynucleotide may also be used in preparing PRO polypeptides by
CC recombinant techniques, and in generating either transgenic animals or
CC knock-out animals which, in turn, are useful in the development and
CC screening of therapeutically useful reagents. The PRO polypeptide or the
CC antibody is used in preparing a medicament for treating a condition
CC responsive to the polypeptide or antibody, such as tumours, and in
CC various diagnostic assays. The present sequence represents a PRO
CC polypeptide
XX
SQ Sequence 586 AA;

Query Match 92.5%; Score 2815; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEIHSMDPCLINENFNEQKVNQEALEILSAITQPVVVAIVGLVTRGKSYLMNKLKAG 60
DB 1 MALEIHSMDPCLINENFNEQKVNQEALEILSAITQPVVVAIVGLVTRGKSYLMNKLKAG 60
QY 61 KNGFSVASTVQSHTKGIWVCVPHNPNHTLVLDTGEGDVEKADNNDIQIFALAL 120
DB 61 KNGFSVASTVQSHTKGIWVCVPHNPNHTLVLDTGEGDVEKADNNDIQIFALAL 120
QY 121 LLSSTFYNTVTKIDQGAIDLLHNVTETDILLKARNSPDLDRVEDPADSASFPDLVWTL 180
DB 121 LLSSTFYNTVTKIDQGAIDLLHNVTETDILLKARNSPDLDRVEDPADSASFPDLVWTL 180
QY 181 RDCFLGLEIDQVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFPFKKCFIFDLPA 240
DB 181 RDCFLGLEIDQVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFPFKKCFIFDLPA 240
QY 241 HQKLAQLETLPDDELEPEFVQVTEFCVIFSHSMTKTLPGGIMVNGSLKMLVLTYN 300
DB 241 HQKLAQLETLPDDELEPEFVQVTEFCVIFSHSMTKTLPGGIMVNGSLKMLVLTYN 300
QY 301 AISSGDLPCINAVLALQRENSAAVQKATAHYDQMGQKQVQLPMETLQELLDLHRTSER 360
DB 301 AISSGDLPCINAVLALQRENSAAVQKATAHYDQMGQKQVQLPMETLQELLDLHRTSER 360
QY 361 EAEVFMKNSFKVDQSFQKELETLDAKNDICKRNLEASSDYCSALLKIDFGPLEEAV 420
DB 361 EAEVFMKNSFKVDQSFQKELETLDAKNDICKRNLEASSDYCSALLKIDFGPLEEAV 420
QY 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
DB 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480

QY 481 TETETKKKKAQVKAEEKAQAQLAAIQRQNEQMMQERLHQSVRQMETAKQNWLAEQ 540
DB 481 TETETKKKKAQVKAEEKAQAQLAAIQRQNEQMMQERLHQSVRQMETAKQNWLAEQ 540
QY 541 QKWQEQQMQ 549
DB 541 QKWQEQQMQ 549
RESULT 9
ABU66868
ID ABU66868 standard; protein; 586 AA.
XX AC ABU66868;
XX DT 27-MAY-2003 (first entry)
XX DE Human secreted/transmembrane, PRO; protein SEQ ID 46.
XX KW Human; secreted protein; transmembrane protein; PRO;
XX KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
XX KW infertility; birth defects; premature aging; AIDS; biosensor;
XX KW acquired immunodeficiency syndrome; cancer; diabetic complication;
XX KW bioreactor; tumour.
XX OS Homo sapiens.
XX PN US2003032155-A1.
XX PD 13-FEB-2003.
XX PF 03-MAY-2002; 2002US-00137865.
XX PR 31-MAR-1997; 97WO-US005230.
XX PR 12-JUN-1998; 98WO-US012456.
XX PR 14-JUL-1998; 98WO-US014552.
XX PR 28-AUG-1998; 98WO-US017888.
XX PR 10-SEP-1998; 98WO-US018824.
XX PR 14-SEP-1998; 98WO-US019093.
XX PR 14-SEP-1998; 98WO-US019094.
XX PR 14-SEP-1998; 98WO-US019177.
XX PR 16-SEP-1998; 98WO-US019330.
XX PR 17-SEP-1998; 98WO-US019437.
XX PR 07-OCT-1998; 98WO-US021141.
XX PR 29-OCT-1998; 98WO-US022991.
XX PR 29-OCT-1998; 98WO-US022992.
XX PR 01-DEC-1998; 98WO-US024855.
XX PR 05-JAN-1999; 99WO-US000106.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 10-MAR-1999; 99WO-US005190.
XX PR 20-APR-1999; 99WO-US008615.
XX PR 14-MAY-1999; 99WO-US010733.
XX PR 01-SEP-1999; 99WO-US020111.
XX PR 08-SEP-1999; 99WO-US020594.
XX PR 13-SEP-1999; 99WO-US020944.
XX PR 15-SEP-1999; 99WO-US021090.
XX PR 15-SEP-1999; 99WO-US021547.
XX PR 05-OCT-1999; 99WO-US023089.
XX PR 29-NOV-1999; 99WO-US028214.
XX PR 30-NOV-1999; 99WO-US028313.
XX PR 01-DEC-1999; 99WO-US028409.
XX PR 01-DEC-1999; 99WO-US028301.
XX PR 02-DEC-1999; 99WO-US028551.
XX PR 02-DEC-1999; 99WO-US028564.
XX PR 02-DEC-1999; 99WO-US028565.
XX PR 16-DEC-1999; 99WO-US030095.
XX PR 20-DEC-1999; 99WO-US030911.
XX PR 20-DEC-1999; 99WO-US030999.
XX PR 22-DEC-1999; 99WO-US030720.

PR 30-DEC-1999; 99WO-US0311243.
 PR 30-DEC-1999; 99WO-US0311274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US0003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US022031.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001US-00802706.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00806889.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI: 2003-331925/31.
 DR N-PSDB; ACA04046.
 DR
 XX New secreted and transmembrane nucleic acids and polypeptides, designated
 PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
 PT cardiac injury, infertility, birth defects, premature aging, AIDS, or

PT cancer.
 XX Claim 12; Fig 46; 659pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid further
 CC comprises the full-length coding sequence of the DNA deposited under
 CC American Type Culture Collection (ATCC) accession number in a list given
 CC in the specification. Also included are vectors and host cells for
 CC producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO
 CC extracellular domains and mature sequences, methods of detecting PRO
 CC proteins, methods for stimulating the release of TNF-alpha (tumour
 CC necrosis factor alpha) from human blood, (and the proliferation of
 CC differentiation of chondrocyte cells, the proliferation of, or gene
 CC expression in pericyte cells, the release of proteoglycans from
 CC cartilage, proliferation of inner ear utricular supporting cells, the
 CC proliferation of T-lymphocyte cells, the release of a cytokine from
 CC peripheral blood mononuclear cells (PBMC), or the proliferation of
 CC endothelial cells), a method for modulating the uptake of glucose or free
 CC fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the
 CC binding of A-peptide to factor VIIA, or the differentiation of adipocyte
 CC cells, a method for detecting the presence of a tumour in a mammal and an
 CC oligonucleotide probe derived from any of the nucleotide sequences cited
 CC above. The nucleic acids and polypeptides are useful for treating
 CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
 CC infertility, birth defects, premature aging, AIDS (acquired
 CC immunodeficiency syndrome), cancer, or diabetic complications. The
 CC nucleic acids are useful as hybridisation probes, in chromosome and gene
 CC mapping, and in generating antisense RNA or DNA. The polypeptides are
 CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both
 CC are useful in tissue typing. The present sequence represents a PRO
 CC protein of the invention
 XX
 SQ Sequence 586 AA;
 Query Match 92.5%; Score 2815; DB 6; Length 586;
 Best Local Similarity 100.0%; Pred. No. 1.2e-222; Indels 0; Gaps 0;
 Matches 549; Conservative 0; Mismatches 0;
 Qy 1 MALEIHMSDPMCLIEFNQKLVNQBALITLTAITQPVVVAIVGLYRTKSLMKNLAG 60
 Db 1 MALEIHMSDPMCLIEFNQKLVNQBALITLTAITQPVVVAIVGLYRTKSLMKNLAG 60
 Qy 61 KXGFSVASTVQSHTKGIWICVPHNPWPHNHTLVLDTEGLGDEVKADNNDIQIFALAL 120
 Db 61 KXGFSVASTVQSHTKGIWICVPHNPWPHNHTLVLDTEGLGDEVKADNNDIQIFALAL 120
 Qy 121 LLSSTFYNTVTKIDQGAIDLHNVTETLTLKARNSPDLDRVEDPADSASFPDLVWTL 180
 Db 121 LLSSTFYNTVTKIDQGAIDLHNVTETLTLKARNSPDLDRVEDPADSASFPDLVWTL 180
 Qy 181 RDFCLGLEIDQLVTPDEVLENSLRPKQSDQVQNFNLRCLCIQKFPFKKCFIDPLPA 240
 Db 181 RDFCLGLEIDQLVTPDEVLENSLRPKQSDQVQNFNLRCLCIQKFPFKKCFIDPLPA 240
 Qy 241 HQKLAQLETLPDDELEPEFVQVTFECSYIFSHSMTKTLPGGIMWNGSLKMLVLYVN 300
 Db 241 HQKLAQLETLPDDELEPEFVQVTFECSYIFSHSMTKTLPGGIMWNGSLKMLVLYVN 300
 Qy 301 AISSGDLPCIENAVLALAORENSAAVQKATAHYDQMGQKVQLPMETLOELDLHRTSER 360
 Db 301 AISSGDLPCIENAVLALAORENSAAVQKATAHYDQMGQKVQLPMETLOELDLHRTSER 360
 Qy 361 EAIEVFMKNSFKDVQDSFQKELETLDDAKONDICKRNLEASSDYCSALLKDKIFGPLEEAV 420
 Db 361 EAIEVFMKNSFKDVQDSFQKELETLDDAKONDICKRNLEASSDYCSALLKDKIFGPLEEAV 420
 Qy 421 KQIYKPGGHNLFIOKTEELKAKYREPRKGIQAEVLOKYLKSKESVSHALLOTOAL 480
 Db 421 KQIYKPGGHNLFIOKTEELKAKYREPRKGIQAEVLOKYLKSKESVSHALLOTOAL 480

QY 481 TETETKKKKAQVKAEEKAQRLAAIQRNEQMMQERRLHQEVQRMEIAKQNWLABQ 540
 DB 481 TETETKKKKAQVKAEEKAQRLAAIQRNEQMMQERRLHQEVQRMEIAKQNWLABQ 540
 QY 541 QKMQEQOQM 549
 DB 541 QKMQEQOQM 549

RESULT 10
 ADA45565
 ID ADA45565 standard; protein; 586 AA.
 XX ADA45565;
 AC ADA45565;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO4987.
 XX
 KW Human; secreted and transmembrane protein; PRO;
 KW Tumour necrosis factor alpha release; TNF-alpha release;
 KW glucose uptake modulator; FFA uptake modulator;
 KW cell proliferation stimulator; cell differentiation stimulator;
 KW cell differentiation inhibitor; cytokine release stimulator; tumour;
 KW lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW cervical tumour; liver tumour; chromosome mapping; gene mapping;
 KW gene therapy; chromosome identification; chromosome marker.
 XX
 OS Homo sapiens.
 XX
 XX
 PN US2003022328-A1.
 XX
 PD 30-JAN-2003.
 XX
 XX 16-APR-2002; 2002US-00123904.
 XX
 PR 31-MAR-1997; 99WO-US005230.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019094.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 29-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 98WO-US000106.
 PR 08-MAR-1999; 98WO-US005028.
 PR 10-MAR-1999; 98WO-US005190.
 PR 20-APR-1999; 98WO-US008615.
 PR 14-MAY-1999; 98WO-US010733.
 PR 02-JUN-1999; 98WO-US012252.
 PR 01-SEP-1999; 98WO-US020111.
 PR 08-SEP-1999; 98WO-US020594.
 PR 13-SEP-1999; 98WO-US020944.
 PR 15-SEP-1999; 98WO-US021090.
 PR 05-OCT-1999; 98WO-US021547.
 PR 29-NOV-1999; 98WO-US023089.
 PR 29-NOV-1999; 98WO-US028214.
 PR 30-NOV-1999; 98WO-US028313.
 PR 30-NOV-1999; 98WO-US028409.
 PR 01-DEC-1999; 98WO-US028301.
 PR 01-DEC-1999; 98WO-US028634.
 PR 02-DEC-1999; 98WO-US028551.
 PR 02-DEC-1999; 98WO-US028564.
 PR 02-DEC-1999; 98WO-US028565.
 PR 16-DEC-1999; 98WO-US030095.
 PR 20-DEC-1999; 98WO-US030911.

PR 20-DEC-1999; 99WO-US030999.
 PR 22-DEC-1999; 99WO-US030720.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015284.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 01-JUN-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 05-JUN-2001; 2001WO-US017800.
 PR 14-JUN-2001; 2001US-00874503.
 PR 19-JUN-2001; 2001US-00882636.
 PR 20-JUN-2001; 2001US-00886342.
 PR 21-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WJ, Zhang Z;
 XX
 DR WPI: 2003-584997/55.
 DR N-PSDB; ADA45564.
 XX
 PT Novel secreted and transmembrane polypeptide for modulating biological

PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.

PS Claim 12; Fig 46; 659pp; English.

XX The invention describes 305 nucleic acids encoding PRO (secreted and
XX transmembrane) polypeptides (I). (I) is useful for stimulating the
CC release of TNF-alpha from human blood, for modulating the uptake of
CC glucose or PFA by skeletal muscle cells or adipocyte cells, for
CC stimulating the proliferation or differentiation of chondrocyte cells,
CC for stimulating the proliferation of or gene expression in pericyte
CC cells, for stimulating the release of proteoglycans from cartilage, for
CC stimulating the proliferation of inner ear utricular supporting cells,
CC for stimulating the proliferation of T-lymphocyte cells, for stimulating
CC the release of a cytokine from BMC cells, for inhibiting the binding of
CC A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte
CC cells, for stimulating proliferation of endothelial cells, for detecting
CC the presence of tumour in a mammal. The tumour is lung, colon, breast,
CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes
CC are useful for isolating genomic and cDNA nucleotide sequences or
CC antisense probes. (I) is also useful as therapeutic agent. PRO is useful
CC in assays to identify other proteins or molecules involved in binding
CC interaction. A polynucleotide (II) encoding (I) is useful in chromosome
CC and gene mapping, in generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptide, for generating transgenic animals or
CC knockout animals which in turn are useful in the development and
CC screening of therapeutically useful reagents, in gene therapy, for
CC chromosome identification, as chromosome marker, and for generating
CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.
CC detecting its expression in specific cells, tissues or serum, and for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. (I) and (II) are useful for tissue typing. This is the amino
CC acid sequence of a novel human secreted and transmembrane PRO
CC polypeptide.

XX Sequence 586 AA;

Query Match		92.5%;	Score 2815;	DB 6;	Length 586;
Best Local Similarity		100.0%;	Pred. No. 1.2e-222;		
Matches 549;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MALETHMSDPMCLINFNQKLVNQAELEILSAITQPVVVAIVGLYRTGSKYLMKVLG	60		
Db	1	MALETHMSDPMCLINFNQKLVNQAELEILSAITQPVVVAIVGLYRTGSKYLMKVLG	60		
QY	61	KNGGSVASTVQSHTKGIWICVPHNPNHTLVLLDTGEGLDVEKADNKNDIQIFALAL	120		
Db	61	KNGGSVASTVQSHTKGIWICVPHNPNHTLVLLDTGEGLDVEKADNKNDIQIFALAL	120		
QY	121	LLSSTFVNTVNNKIDQGAIDLHNVTETDLLKARNSPDLRVEDPADSAGFPDLVWTL	180		
Db	121	LLSSTFVNTVNNKIDQGAIDLHNVTETDLLKARNSPDLRVEDPADSAGFPDLVWTL	180		
QY	181	RDFCLGLEIDGLVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFFPKKCFIFDLPA	240		
Db	181	RDFCLGLEIDGLVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFFPKKCFIFDLPA	240		
QY	241	HOKKLAQLETLDDLEPEFVQVTEFCSYIIFSHSMTKTLPGGIMVNGSRLLKVLTVYN	300		
Db	241	HOKKLAQLETLDDLEPEFVQVTEFCSYIIFSHSMTKTLPGGIMVNGSRLLKVLTVYN	300		
QY	301	ATSSGDLPCINAVLALAQRENSAAVQKAIAYHDQMGOKVQLPMETLQELLDLHRTSER	360		
Db	301	ATSSGDLPCINAVLALAQRENSAAVQKAIAYHDQMGOKVQLPMETLQELLDLHRTSER	360		
QY	361	EAIEVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKRNLEASSDYCSALLKIDIFGPLEEAV	420		
Db	361	EAIEVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKRNLEASSDYCSALLKIDIFGPLEEAV	420		
QY	421	KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHALLOTDOAL	480		
Db	421	KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHALLOTDOAL	480		

QY	481	TETETKKKKEAQVKAEBKAQAORLAAIQRONEQMMQERLHQVQVQMETAKQNWLAEQ	540		
Db	481	TETETKKKKEAQVKAEBKAQAORLAAIQRONEQMMQERLHQVQVQMETAKQNWLAEQ	540		
QY	541	QKMQEQQQMQ	549		
Db	541	QKMQEQQQMQ	549		
RESULT 11					
ADA75996					
ID	ADA75996	standard; protein; 586 AA.			
XX					
AC	ADA75996;				
XX					
DT	20-NOV-2003	(first entry)			
XX					
DE	Human PRO polypeptide #23.				
XX					
KW	Human; PRO; secreted polypeptide; transmembrane polypeptide;				
KW	tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;				
KW	cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;				
KW	liver; microvascular endothelial cell; glucose; PFA;				
KW	skeletal muscle cell; adipocyte cell; pericyte cell;				
KW	inner ear utricular supporting cell; T-lymphocyte cell;				
KW	endothelial cell tube formation; bone disorder; cartilage disorder;				
KW	sports injury; proteoglycan; articular cartilage defect; osteoarthritis;				
KW	rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;				
KW	immune system cell infiltration.				
XX					
OS	Homo sapiens.				
XX					
PN	US2003073212-A1.				
XX					
PD	17-APR-2003.				
XX					
PF	16-APR-2002; 2002US-00123903.				
XX					
PR	31-MAR-1997; 97WO-US005230.				
PR	12-JUN-1998; 98WO-US012456.				
PR	14-JUL-1998; 98WO-US014552.				
PR	28-AUG-1998; 98WO-US017888.				
PR	10-SEP-1998; 98WO-US018624.				
PR	14-SEP-1998; 98WO-US019093.				
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PR	14-SEP-1998; 98WO-US019177.				
PR	16-SEP-1998; 98WO-US019330.				
PR	17-SEP-1998; 98WO-US019437.				
PR	07-OCT-1998; 98WO-US021141.				
PR	29-OCT-1998; 98WO-US022991.				
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PR	20-NOV-1998; 98WO-US024855.				
PR	01-DEC-1998; 98WO-US025108.				
PR	05-JAN-1999; 98WO-US000106.				
PR	08-MAR-1999; 99WO-US005028.				
PR	10-MAR-1999; 99WO-US005190.				
PR	20-APR-1999; 99WO-US008615.				
PR	14-MAY-1999; 99WO-US010733.				
PR	02-JUN-1999; 99WO-US012252.				
PR	01-SEP-1999; 99WO-US020111.				
PR	08-SEP-1999; 99WO-US020594.				
PR	13-SEP-1999; 99WO-US020944.				
PR	15-SEP-1999; 99WO-US021090.				
PR	15-SEP-1999; 99WO-US021547.				
PR	05-OCT-1999; 99WO-US023089.				
PR	29-NOV-1999; 99WO-US028214.				
PR	30-NOV-1999; 99WO-US028313.				
PR	30-NOV-1999; 99WO-US028409.				
PR	01-DEC-1999; 99WO-US028301.				
PR	01-DEC-1999; 99WO-US028634.				
PR	02-DEC-1999; 99WO-US028551.				
PR	02-DEC-1999; 99WO-US028564.				
PR	02-DEC-1999; 99WO-US028565.				


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PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004934.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030932.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019632.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
PA (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-687639/65.
DR N-PSDB; ADA75995.
```

XX New isolated nucleic acid encoding a secreted and transmembrane
PT polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and
PT gene mapping, in generating antisense RNA and DNA, and in gene therapy.
XX
PS Claim 12; Fig 46; 659pp; English.
XX
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating differentiation of adipocyte cells, for stimulating
CC the proliferation of or gene expression in pericyte cells, for stimulating
CC the proliferation of inner ear utricular supporting cells or T-lymphocyte
CC cells, for inducing endothelial cell tube formation and for treating
CC various bone and/or cartilage disorders such as sports injuries and
CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
CC from cartilage are useful for treating sports-related joint problems,
CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
CC polypeptides are also useful for treating various mammalian haemoglobin-
CC associated disorders such as various thalassaemias and conditions which
CC may benefit from enhanced local immune system cell infiltration. This
CC sequence represents a human PRO polypeptide of the invention. Note: The
CC sequence data for this patent is also available in electronic format from
CC USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 586 AA;

Query Match 92.5%; Score 2815; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEIHMSDPNCLIEFNEQIKVNOEALIEILSAITQPVVVAIVGLYRTGSKYLNKLAG 60
Db 1 MALEIHMSDPNCLIEFNEQIKVNOEALIEILSAITQPVVVAIVGLYRTGSKYLNKLAG 60
Qy 61 KNKGFSVASTVQSHTKGIWICVPHNPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db 61 KNKGFSVASTVQSHTKGIWICVPHNPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
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Db 121 LLSSTFFVNTVKNIDQGAIDLHNVTELTDLKARNSPDLDRVEDPADSADFFPDVWTL 180
Qy 181 RDFCLGLEIDQVLPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFPKKCFDPLPA 240
Db 181 RDFCLGLEIDQVLPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFPKKCFDPLPA 240
Qy 241 HQKLAQLETLDPDDELEPEFVQQTVEFCSYFFSHSMTKLPCGIMVNGSRKLNVLTVYN 300
Db 241 HQKLAQLETLDPDDELEPEFVQQTVEFCSYFFSHSMTKLPCGIMVNGSRKLNVLTVYN 300
Qy 301 AISSGDLPCIEAVLALAQRENSAAVQKAIHYDQMGQKQVQLPMETLQELLDLHRTSER 360
Db 301 AISSGDLPCIEAVLALAQRENSAAVQKAIHYDQMGQKQVQLPMETLQELLDLHRTSER 360
Qy 361 EAEIVFMKNSFKVDQSFQKELETILLDAKNDIDCKRNLEASSDYCSALLKIDIFGPLEAV 420
Db 361 EAEIVFMKNSFKVDQSFQKELETILLDAKNDIDCKRNLEASSDYCSALLKIDIFGPLEAV 420

Db 361 EAIEVFMKNSFKVDQSFQKLETLLDQAKQNDICRNLDASSDYCSALLKDFGPLEEAV 420
ADAL8646
Oy 421 KOGIYKPGGHNLFQKTEELKAKYRPRKGIQAEVLQYKLSKESVSHAILQTDQAL 480
Db 421 KOGIYKPGGHNLFQKTEELKAKYRPRKGIQAEVLQYKLSKESVSHAILQTDQAL 480
Oy 481 TETEKKKKAEQVKAERAEKAEQRLAAIORQNEQMMQERERLHQEQVQRMETAKQNWLAEQ 540
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Oy 541 QKMQEQQMQ 549
Db 541 QKMQEQQMQ 549
RESULT 12
ID ADA18646 standard; protein; 586 AA.
XX
AC ADA18646;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human PRO polypeptide #23.
XX
KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; lung;
KW colon; breast; prostate; rectum; cervix; liver; tumour; cancer;
KW glucose uptake; FFA; adipocyte cell; pericyte cell; proteoglycan;
KW cartilage; inner ear utricular supporting cell; cytokine; A-peptide;
KW factor VIIA; endothelial cell.
XX
OS Homo sapiens.
XX
PN US2003054517-Al.
XX
PD 20-MAR-2003.
XX
PF 08-MAY-2002; 2002US-00141755.
XX
XX 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 10-MAR-1999; 98WO-US005190.
PR 20-APR-1999; 98WO-US008615.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 01-SEP-1999; 98WO-US020111.
PR 08-SEP-1999; 98WO-US020594.
PR 13-SEP-1999; 98WO-US020944.
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PR 05-OCT-1999; 98WO-US023089.
PR 29-NOV-1999; 98WO-US028214.
PR 30-NOV-1999; 98WO-US028313.
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PR 01-DEC-1999; 98WO-US028301.
PR 01-DEC-1999; 98WO-US028634.
PR 02-DEC-1999; 98WO-US028551.

PR 02-DEC-1999; 99WO-US028564.
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PR 20-DEC-1999; 99WO-US030911.
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PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 10-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006319.
PR 20-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006566.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001WO-US017092.
PR 25-MAY-2001; 2001US-00866034.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
XX

DR WPI: 2003-521854/49.
DR N-PSDB; ADA18645.
XX New PRO nucleic acid, useful for preparing a composition for treating
PT e.g., tumors.
XX
XX Claim 12; Fig 46; 660pp; English.
XX
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
CC prostate, cervical and liver tumours). The polynucleotides are
CC useful in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA and in
CC gene therapy. The polynucleotides may also be used in preparing PRO
CC polypeptides by recombinant techniques and in generating either
CC transgenic animals or knock-out animals which are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptides or antibodies are used in preparing a medicament for
CC treating a condition responsive to the polypeptides or antibodies, such
CC as tumours, for modulating the uptake of glucose or FFA by adipocyte
CC cells, for stimulating the proliferation of or gene expression in
CC pericyte cells, for stimulating the release of proteoglycans from
CC cartilage, for stimulating the proliferation of inner ear utricular
CC supporting cells, for stimulating the release of cytokines from PBMC
CC cells, for inhibiting the binding of A-peptide to factor VIIA, for
CC inhibiting the differentiation of adipocyte cells and for stimulating the
CC proliferation of endothelial cells. This sequence represents a human PRO
CC polypeptide of the invention. Note: The sequence data for this patent is
CC also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
XX Sequence 586 AA;

Query Match 92.5%; Score 2815; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALETHMSDPMCLIEFNELKQVQAEILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60
DB 1 MALETHMSDPMCLIEFNELKQVQAEILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60
QY 61 KNGGFSVASTVQSHTKGIWVCVPHNPNHTLVLLDTGGLGDKVKAQNDIQIFALAL 120
DB 61 KNGGFSVASTVQSHTKGIWVCVPHNPNHTLVLLDTGGLGDKVKAQNDIQIFALAL 120
QY 121 LLSSTFVYNTVTKIDQGAIDLHNVTETDLKARNSPDLDRVEDPADSASFPDLVWTL 180
DB 121 LLSSTFVYNTVTKIDQGAIDLHNVTETDLKARNSPDLDRVEDPADSASFPDLVWTL 180
QY 181 RDPCLGLEIDGQVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFPFKKCFIPDLPA 240
DB 181 RDPCLGLEIDGQVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFPFKKCFIPDLPA 240
QY 241 HOKKLAQLETLPPDELEPFVQVTFECSYIIFSHSMTKTLPGIMVNGSRLKNLVITYN 300
DB 241 HOKKLAQLETLPPDELEPFVQVTFECSYIIFSHSMTKTLPGIMVNGSRLKNLVITYN 300
QY 301 AISSGDLPCIEANVALAQAENSAAVQKAIHYDQMGOKVQLPMETLQELLDLHRTSER 360
DB 301 AISSGDLPCIEANVALAQAENSAAVQKAIHYDQMGOKVQLPMETLQELLDLHRTSER 360
QY 361 EAIEVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKNSDYCSALLKDIIFGPLEAV 420
DB 361 EAIEVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKNSDYCSALLKDIIFGPLEAV 420
QY 421 KOGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
DB 421 KOGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480

QY 481 TETETKKKEAQVKAEBKAEKAEQRLAAIQRONQMMQERRLHQBQVRQNEIAKQNWLAQ 540
DB 481 TETETKKKEAQVKAEBKAEKAEQRLAAIQRONQMMQERRLHQBQVRQNEIAKQNWLAQ 540
QY 541 QKMQEQQQMQ 549
DB 541 QKMQEQQQMQ 549
RESULT 13
ADA61269
ID ADA61269 standard; protein; 586 AA.
XX ADA61269;
AC ADA61269;
DT 20-NOV-2003 (first entry)
XX Homo sapiens.
XX Human; secreted and transmembrane protein; PRO;
KW Tumour necrosis factor alpha release; TNF-alpha release;
KW glucose uptake modulator; FFA uptake modulator;
KW cell proliferation stimulator; cell differentiation stimulator;
KW cell differentiation inhibitor; cytokine release stimulator; tumour;
KW lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; chromosome mapping; gene mapping;
KW gene therapy; chromosome identification; chromosome marker.
XX Novel.
OS human.
OS secreted.
OS and.
OS transmembrane.
OS protein.
OS PRO4987.
XX US2003049816-A1.
XX 13-MAR-2003.
XX 15-APR-2002; 2002US-00123262.
XX 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 10-MAR-1999; 98WO-US005190.
PR 20-APR-1999; 98WO-US008615.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 01-SEP-1999; 98WO-US020111.
PR 08-SEP-1999; 98WO-US020594.
PR 13-SEP-1999; 98WO-US020944.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.
PR 05-OCT-1999; 98WO-US023089.
PR 29-NOV-1999; 98WO-US028214.
PR 30-NOV-1999; 98WO-US028313.
PR 30-NOV-1999; 98WO-US028409.

PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US003376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;

PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI: 2003-695892/66.
DR N-PSDB; ADA61268.
XX
PT New PRO nucleic acid and encode polypeptides, are useful for
PT manufacturing a medicament for diagnosing or treating cancer.
XX
PS Claim 12; Fig 46; 660pp; English.

CC The invention describes 305 nucleic acids encoding PRO (secreted and
CC transmembrane) polypeptides (I). (I) is useful for stimulating the
CC release of TNF-alpha from human blood, for modulating the uptake of
CC glucose or PFA by skeletal muscle cells or adipocyte cells, for
CC stimulating the proliferation or differentiation of chondrocyte cells,
CC for stimulating the proliferation of or gene expression in pericyte
CC cells, for stimulating the release of proteoglycans from cartilage, for
CC stimulating the proliferation of inner ear utricular supporting cells,
CC stimulating the proliferation of T-lymphocyte cells, for stimulating
CC the release of a cytokine from BMC cells, for inhibiting the binding of
CC A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte
CC cells, for stimulating proliferation of endothelial cells, for detecting
CC the presence of tumour in a mammal. The tumour is lung, colon, breast,
CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes
CC are useful for isolating genomic and cDNA nucleotide sequences or
CC antisense probes. (I) is also useful as therapeutic agent. PRO is useful
CC in assays to identify other proteins or molecules involved in binding
CC interaction. A polynucleotide (II) encoding (I) is useful in chromosome
CC and gene mapping, in generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptide, for generating transgenic animals or
CC knockout animals which in turn are useful in the development and
CC screening of therapeutically useful reagents, in gene therapy, for
CC chromosome identification, as chromosome marker, and for generating
CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.
CC detecting its expression in specific cells, tissues or serum, and for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. (I) and (II) are useful for tissue typing. This is the amino
CC acid sequence of a novel human secreted and transmembrane PRO
CC polypeptide.

XX SQ Sequence 586 AA;

Query Match 92.5%; Score 2815; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.2e-322;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEIHMSDPMCLIENTNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKL 60
Db 1 MALEIHMSDPMCLIENTNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKL 60
Qy 61 KNGGFSVASTVQSHTKGIWICVPHNPNHTLVLLDTEGIDVEKADKNNDIOIFALAL 120
Db 61 KNGGFSVASTVQSHTKGIWICVPHNPNHTLVLLDTEGIDVEKADKNNDIOIFALAL 120
Qy 121 LLSSTFYVNTVKNIDQCAIDLLHNVTETDILLKARNSPDLDRVEDPADSASFFDLVWTL 180
Db 121 LLSSTFYVNTVKNIDQCAIDLLHNVTETDILLKARNSPDLDRVEDPADSASFFDLVWTL 180
Qy 181 RDFCLGLEIDQVLPDEYLENSLRPKGSDQRQVNFNLPRLCIQKFPKPKKCFIDLPA 240
Db 181 RDFCLGLEIDQVLPDEYLENSLRPKGSDQRQVNFNLPRLCIQKFPKPKKCFIDLPA 240
Qy 241 HQKLAQLETPDDELEPEFVQVTEFCSYIFSHMTKTLPGGIMVNGSRUKNLVLTVN 300
Db 241 HQKLAQLETPDDELEPEFVQVTEFCSYIFSHMTKTLPGGIMVNGSRUKNLVLTVN 300
Qy 301 AISSGDLPCIEAVLALAQRENSAAVQKAIHAHYDQMGQKQVQLPMTETIQELDLHRTSER 360
Db 301 AISSGDLPCIEAVLALAQRENSAAVQKAIHAHYDQMGQKQVQLPMTETIQELDLHRTSER 360
Qy 361 EAIFFVMKNSPKVDVQSFQKELETLLDAKNDICRNLKLEASSDYCSALLKDIQFPLEBAV 420
Db 361 EAIFFVMKNSPKVDVQSFQKELETLLDAKNDICRNLKLEASSDYCSALLKDIQFPLEBAV 420

Db 361 EAIEVFMKNSPKVDOSFQKELETLDDAKQNDICKRNLEASSDYCSALLKIDIFGPLEAV 420
Qy 421 KGIYSKPGCHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
Db 421 KGIYSKPGCHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
Qy 481 TETEKKKKAQVKAEEAQAORLAAIQRONEQMMQERLHQRONEIAKQNLAAQ 540
Db 481 TETEKKKKAQVKAEEAQAORLAAIQRONEQMMQERLHQRONEIAKQNLAAQ 540
Qy 541 QRMQEQQM 549
Db 541 QRMQEQQM 549

RESULT 14
ADBI9054
ID ADBI9054 standard; protein; 586 AA.
XX
AC ADBI9054;
XX
DT 20-NOV-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO4987.
XX
KW Human; secreted and transmembrane protein; PRO;
KW Tumour necrosis factor alpha release; TNF-alpha release;
KW glucose uptake modulator; FFA uptake modulator;
KW cell proliferation stimulator; cell differentiation stimulator;
KW cell differentiation inhibitor; cytokine release.
XX
OS Homo sapiens.
XX
PN US2003068796-A1.
XX
PD 10-APR-2003.
XX
PF 15-APR-2002; 2002US-00123261.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028401.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
WPI; 2003-695927/66.

DR N-PSDB; ADB19053.
XX Novel secreted and transmembrane PRO polypeptides useful for stimulating
PT the release of tumor necrosis factor alpha and detecting the presence of
PT a tumor in a mammal.
XX Claim 12; Fig 46; 660pp; English.
XX
XX The invention describes 305 nucleic acids encoding PRO (secreted and
CC transmembrane) polypeptides (I). (I) is useful for stimulating the
CC release of TNF-alpha from human blood, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte
XX Sequence 586 AA;
SQ

Query Match 92.5%; Score 2815; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEIHSMDPCLNENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLGA 60
Db 1 MALEIHSMDPCLNENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLGA 60
QY 61 KNGGFSVASTVQSHTKGIWICVPHPNPNHTLVLLDTEGLGDEVEKADKNNDIQIFALAL 120
Db 61 KNGGFSVASTVQSHTKGIWICVPHPNPNHTLVLLDTEGLGDEVEKADKNNDIQIFALAL 120
QY 121 LLSSTFVYNTVNTKIDQGAIDLHNVTETDLKARNSPDLRVEDPADSASFFPDVWTL 180
Db 121 LLSSTFVYNTVNTKIDQGAIDLHNVTETDLKARNSPDLRVEDPADSASFFPDVWTL 180
QY 181 RDFCLGLEIDGOLVTPDDEYLENSLRPKQSGDQVQNFNLPRLCIQKPPKKCFIDLPA 240
Db 181 RDFCLGLEIDGOLVTPDDEYLENSLRPKQSGDQVQNFNLPRLCIQKPPKKCFIDLPA 240
QY 241 HQKLAQLETLDPDELEPEFVQVTEFCYSIFSHSMTKTLPGGIWNGSRKLNVLVTYN 300
Db 241 HQKLAQLETLDPDELEPEFVQVTEFCYSIFSHSMTKTLPGGIWNGSRKLNVLVTYN 300
QY 301 AISSGDLPCIEANVLALAQRENSAOKIAHYDQOQGVOLPMTLOEILLDLHRTSER 360
Db 301 AISSGDLPCIEANVLALAQRENSAOKIAHYDQOQGVOLPMTLOEILLDLHRTSER 360
QY 361 EAIEVFMKNSFKVDVDSQFKELETLDDAKNDICRNLKNSDYCSALLKIDIFGPLEAV 420
Db 361 EAIEVFMKNSFKVDVDSQFKELETLDDAKNDICRNLKNSDYCSALLKIDIFGPLEAV 420
QY 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVYLQYLSKESVSHAILQTDQAL 480
Db 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVYLQYLSKESVSHAILQTDQAL 480
QY 481 TETEKKEAQAQKAEAEQAORLAAIQORNEQMOERLHOBQVROMETAKQNWLAEQ 540
Db 481 TETEKKEAQAQKAEAEQAORLAAIQORNEQMOERLHOBQVROMETAKQNWLAEQ 540
QY 541 QRMQEQQMQ 549
Db 541 QRMQEQQMQ 549

RESULT 15
ADB27595
ID ADB27595 standard; protein; 586 AA.
XX
AC ADB27595;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human PRO polypeptide #23.
XX
KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
KW cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;

KW liver; microvascular endothelial cell; glucose; FFA;
KW skeletal muscle cell; adipocyte cell; pericyte cell;
KW inner ear utricular supporting cell; T-lymphocyte cell;
KW endothelial cell tube formation; bone disorder; cartilage disorder;
KW sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;
KW immune system cell infiltration.
XX Homo sapiens.
OS
XX US2003082704-A1.
PN
XX 01-MAY-2003.
PD
XX
XX 24-APR-2002; 2002US-00131819.
XX
XX 09-DEC-1999; 99US-0170262P.
PR
XX 01-DEC-2000; 2000WO-US032678.
PR
XX 19-DEC-2001; 2001US-00028072.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-765415/72.
DR N-PSDB; ADB27594.
XX
XX New PRO nucleic acid, useful for preparing a composition for treating
PT e.g., tumor or for tissue typing.
XX
XX Claim 12; Fig 46; 637pp; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating differentiation of adipocyte cells, for stimulating
CC the proliferation of or gene expression in pericyte cells, for stimulating
CC the proliferation of inner ear utricular supporting cells or T-lymphocyte
CC cells, for inducing endothelial cell tube formation and for treating
CC various bone and/or cartilage disorders such as sports injuries and
CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
CC from cartilage are useful for treating sports-related joint problems, PRO
CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
CC polypeptides are also useful for treating various mammalian haemoglobin-
CC associated disorders such as various thalassaemias and conditions which
CC may benefit from enhanced local immune system cell infiltration. This
CC sequence represents a human PRO polypeptide of the invention. Note: The
CC sequence data for this patent is also available in electronic format from
CC the USPTO website at segdata.uspto.gov.
XX
SQ Sequence 586 AA;

Query Match 92.5%; Score 2815; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEIHMSDPMCLIEHNFENQKVNQEALEILSAITOPVVVVAIVGLYRTGKSYLANKLAG 60
Db |||||
Qy 1 MALEIHMSDPMCLIEHNFENQKVNQEALEILSAITOPVVVVAIVGLYRTGKSYLANKLAG 60
Db |||||
Qy 61 KNGKFSVASTVQSHTKGIWICVPHNPNHTLVLLDTEGLGDKVEKADNKNNDIQIFALAL 120
Db |||||
Qy 61 KNGKFSVASTVQSHTKGIWICVPHNPNHTLVLLDTEGLGDKVEKADNKNNDIQIFALAL 120
Db |||||
Qy 121 LLSSTFVYNTVANKIDQGAIDLHNVTETLTLKARNSPDLDRVEDPADSASFFPDLVWTL 180
Db |||||
Qy 121 LLSSTFVYNTVANKIDQGAIDLHNVTETLTLKARNSPDLDRVEDPADSASFFPDLVWTL 180
Db |||||
Qy 181 RUPCIGLEIDGQVTPDEYLENSLRPKQSDQORVQNFNLPRLCIQKFFPKKCFIFDLPA 240
Db |||||
Qy 181 RUPCIGLEIDGQVTPDEYLENSLRPKQSDQORVQNFNLPRLCIQKFFPKKCFIFDLPA 240
Db |||||
Qy 241 HQKLAQLETLPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLYVN 300
Db |||||
Qy 241 HQKLAQLETLPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLYVN 300
Db |||||
Qy 301 AISSGDLPCIEHAVLALAQRENSAAVOKAIAHYDQMGQKVQLPMTLQELLDLHRTSER 360
Db |||||
Qy 301 AISSGDLPCIEHAVLALAQRENSAAVOKAIAHYDQMGQKVQLPMTLQELLDLHRTSER 360
Db |||||
Qy 361 EAEVFMKNSFKVDQSFQKELETLDDAKQNDICKRNLEASSDYCSALLKDI FGPLEEAV 420
Db |||||
Qy 361 EAEVFMKNSFKVDQSFQKELETLDDAKQNDICKRNLEASSDYCSALLKDI FGPLEEAV 420
Db |||||
Qy 421 KOGIYSKPGGHNLFQKTEELKAKYREPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
Db |||||
Qy 421 KOGIYSKPGGHNLFQKTEELKAKYREPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
Db |||||
Qy 481 TETEKKKKEAQVKAERKAEQAORLAAIORQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
Db |||||
Qy 481 TETEKKKKEAQVKAERKAEQAORLAAIORQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
Db |||||
Qy 541 QXMQEQQM 549
Db |||||
Qy 541 QXMQEQQM 549
Db |||||

Search completed: July 9, 2005, 13:25:22
Job time : 171 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 13:25:55 ; Search time 162 Seconds
(without alignments)
1409.390 Million cell updates/sec

Title: US-10-659-549-3

Perfect score: 3043

Sequence: 1 MALETHMSDPMCLIEFNEQ.....GEAARSCGQGVNSQKVVV 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1726216 seqs, 386330316 residues

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3043	100.0	591	16	US-10-659-549-3
2	2815	92.5	586	14	US-10-028-072-46
3	2815	92.5	586	14	US-10-140-808-46
4	2815	92.5	586	14	US-10-121-049-46
5	2815	92.5	586	14	US-10-123-904-46
6	2815	92.5	586	14	US-10-140-470-46
7	2815	92.5	586	14	US-10-175-746-46
8	2815	92.5	586	14	US-10-176-918-46
9	2815	92.5	586	14	US-10-176-921-46
10	2815	92.5	586	14	US-10-137-865-46
11	2815	92.5	586	14	US-10-140-474-46

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12 2815 92.5 586 14 US-10-142-431-46
13 2815 92.5 586 14 US-10-143-114-46
14 2815 92.5 586 14 US-10-142-419-46
15 2815 92.5 586 14 US-10-123-262-46
16 2815 92.5 586 14 US-10-142-423-46
17 2815 92.5 586 14 US-10-121-050-46
18 2815 92.5 586 14 US-10-141-755-46
19 2815 92.5 586 14 US-10-143-032-46
20 2815 92.5 586 14 US-10-123-108-46
21 2815 92.5 586 14 US-10-123-236-46
22 2815 92.5 586 14 US-10-123-261-46
23 2815 92.5 586 14 US-10-140-921-46
24 2815 92.5 586 14 US-10-140-928-46
25 2815 92.5 586 14 US-10-121-045-46
26 2815 92.5 586 14 US-10-123-292-46
27 2815 92.5 586 14 US-10-123-903-46
28 2815 92.5 586 14 US-10-124-819-46
29 2815 92.5 586 14 US-10-124-822-46
30 2815 92.5 586 14 US-10-140-925-46
31 2815 92.5 586 14 US-10-160-498-46
32 2815 92.5 586 14 US-10-124-824-46
33 2815 92.5 586 14 US-10-127-825A-46
34 2815 92.5 586 14 US-10-127-829A-46
35 2815 92.5 586 14 US-10-127-835A-46
36 2815 92.5 586 14 US-10-127-839A-46
37 2815 92.5 586 14 US-10-127-901A-46
38 2815 92.5 586 14 US-10-128-693A-46
39 2815 92.5 586 14 US-10-131-813A-46
40 2815 92.5 586 14 US-10-131-818A-46
41 2815 92.5 586 14 US-10-131-823A-46
42 2815 92.5 586 14 US-10-131-830A-46
43 2815 92.5 586 14 US-10-131-837A-46
44 2815 92.5 586 14 US-10-137-872A-46
45 2815 92.5 586 14 US-10-137-872A-46

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ALIGNMENTS

```

RESULT 1
US-10-659-549-3
; Sequence 3, Application US/10659549
; Publication No. US20040229307A1
; GENERAL INFORMATION:
; APPLICANT: Diane Pennica
; TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinFatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/659,549
; FILING DATE: 10-Sep-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,089A
; FILING DATE: 29-Jan-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28 616
; REFERENCE/DOCKET NUMBER: P1056
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881

```

```

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-659-549-3

Query Match      100.0%; Score 3043; DB 16; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.3e-213;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALETHSDPCLTENFNEQLKVNQEALEIISAITQPVVVAIVGLVYRTGKSYLMNKLGA 60
Db 1 MALETHSDPCLTENFNEQLKVNQEALEIISAITQPVVVAIVGLVYRTGKSYLMNKLGA 60

QY 61 KNGGFSVASTVQSHTKGIWICVPHPNWPNHTLVLLDTEGLGDVEKADKNNDIQIFALAL 120
Db 61 KNGGFSVASTVQSHTKGIWICVPHPNWPNHTLVLLDTEGLGDVEKADKNNDIQIFALAL 120

QY 121 LLSSTFVNTYNTKIDQGAIDILHNVTETDILLKARNSPDLDRVEDPADSASFEDLVWTL 180
Db 121 LLSSTFVNTYNTKIDQGAIDILHNVTETDILLKARNSPDLDRVEDPADSASFEDLVWTL 180

QY 181 RDFCLGLIEDGLVTPDDEYLENSLRPKQSGDQRVQNFNPLRLCIQKPPKKKCFIFDLPA 240
Db 181 RDFCLGLIEDGLVTPDDEYLENSLRPKQSGDQRVQNFNPLRLCIQKPPKKKCFIFDLPA 240

QY 241 HQKLAQLLETLPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWVNGSRKLNVLVTYVN 300
Db 241 HQKLAQLLETLPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWVNGSRKLNVLVTYVN 300

QY 301 AISSGDLPCIEAVLALAQRENSAAVQKAIHYDQMGQKQVQLPMETLQELLDLHRTSER 360
Db 301 AISSGDLPCIEAVLALAQRENSAAVQKAIHYDQMGQKQVQLPMETLQELLDLHRTSER 360

QY 361 EAIEVFMKNSFKVDQSFQKELETLLDAKNDICRNLKASDDYCSALLKIDFGPLEEAV 420
Db 361 EAIEVFMKNSFKVDQSFQKELETLLDAKNDICRNLKASDDYCSALLKIDFGPLEEAV 420

QY 421 KQGIYKPGGHNLFQKTEELKAKYRPRKGIQAEVLYQYLKSKESVSHAILQTDQAL 480
Db 421 KQGIYKPGGHNLFQKTEELKAKYRPRKGIQAEVLYQYLKSKESVSHAILQTDQAL 480

QY 481 TETEKKKGAQVKAFAEKAQRLAIIQROEQMMQERLHQBQVQRMETAKQNWLAEQ 540
Db 481 TETEKKKGAQVKAFAEKAQRLAIIQROEQMMQERLHQBQVQRMETAKQNWLAEQ 540

QY 541 QKMQEQQMQVFINCFISPLPTVMRVCCSGKEGAARSQSGQGVWSQKVVV 591
Db 541 QKMQEQQMQVFINCFISPLPTVMRVCCSGKEGAARSQSGQGVWSQKVVV 591

RESULT 2
US-10-028-072-46
; Sequence 46, Application US/10028072
; Publication No. US20030004311a1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059836
; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062285
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062814
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/062816
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063045
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; PRIOR APPLICATION NUMBER: 60/063082
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; PRIOR APPLICATION NUMBER: 60/063127
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063327
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063329
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; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063704
; PRIOR FILING DATE: 1997-10-29
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; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063735
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063738
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064248
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/064809
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065846
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066453
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069212
; PRIOR FILING DATE: 1997-12-11
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; PRIOR FILING DATE: 1997-12-16
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; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: 60/073612
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: 60/074086
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074092
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081695
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081818
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
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; PRIOR APPLICATION NUMBER: 60/083545
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; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
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; PRIOR FILING DATE: 1998-05-13
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; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086414
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086430
; PRIOR FILING DATE: 1998-05-22

; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088730
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088741
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
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; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match 92.5%; Score 2815; DB 14; Length 586;

Best Local Similarity 100.0%; Pred. No. 9.9e-197;

Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MALEIHMSPMCLIEFNFOALQKYNQEALETLSAITOPVVVAIVGLVYRTGKSYLMNKLKAG	60
Db	1	MALEIHMSPMCLIEFNFOALQKYNQEALETLSAITOPVVVAIVGLVYRTGKSYLMNKLKAG	60
Qy	61	KNKGFVASTVQSHTKGIWICVPHNPNHNLVLLDTEGLGDEKADKNDIQIFALAL	120
Db	61	KNKGFVASTVQSHTKGIWICVPHNPNHNLVLLDTEGLGDEKADKNDIQIFALAL	120
Qy	121	LLSSTFYNTVTKIDOGAIDLLHNVTETDOLLKARNSPDLORVEDPADSASFFPDLVWTL	180
Db	121	LLSSTFYNTVTKIDOGAIDLLHNVTETDOLLKARNSPDLORVEDPADSASFFPDLVWTL	180
Qy	181	RDFCLGLEIDGQLVTPDEYLENSLRPKQSDQVQNFNLPRLCTIQKFFPKKCFIFDLPA	240
Db	181	RDFCLGLEIDGQLVTPDEYLENSLRPKQSDQVQNFNLPRLCTIQKFFPKKCFIFDLPA	240
Qy	241	HQKLAQLETLPDDELEPEFVQVTFCSYIFSHSMTKTLPGGIMVNGSLKXNLVLYVN	300
Db	241	HQKLAQLETLPDDELEPEFVQVTFCSYIFSHSMTKTLPGGIMVNGSLKXNLVLYVN	300
Qy	301	AISSGDLPCIEAVLALAQRENSAAVQKAIHAHYDQMGQKQVLPFMTLQBLDLHRTSER	360
Db	301	AISSGDLPCIEAVLALAQRENSAAVQKAIHAHYDQMGQKQVLPFMTLQBLDLHRTSER	360
Qy	361	EATFVFMKNSFKDQVDSFQKLETLDDAKQNDICRKNLEASSDYCSALLDIQFPLEAV	420
Db	361	EATFVFMKNSFKDQVDSFQKLETLDDAKQNDICRKNLEASSDYCSALLDIQFPLEAV	420
Qy	421	KQGIYSKPGGHNLFIQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSMAILQTOQAL	480
Db	421	KQGIYSKPGGHNLFIQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSMAILQTOQAL	480

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Qy 481 TETETKKKKAQVKAERKAEQAORLAALAIQRQNEQMMQERERLHQBQVQVQMEIAKQNWLAEQ 540
Db 481 TETETKKKKAQVKAERKAEQAORLAALAIQRQNEQMMQERERLHQBQVQVQMEIAKQNWLAEQ 540
Qy 541 QKMQEQQM 549
Db 541 QKMQEQQM 549

RESULT 3
US-10-140-808-46
; Sequence 46, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.9e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEIHMSDPMCLLENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
Db 1 MALEIHMSDPMCLLENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
Qy 61 KNGGFSVASTVQSHTKGIWICVPHPNWPNHNTLVLLDTEGLGDVEKADNKNNDIQIFALAL 120
Db 61 KNGGFSVASTVQSHTKGIWICVPHPNWPNHNTLVLLDTEGLGDVEKADNKNNDIQIFALAL 120
Qy 121 LLSTFTYNTVNTKIDQAGAILLHNVTETLTLKARNSPDLDRVEDPADSASFPPDLVWTL 180
Db 121 LLSTFTYNTVNTKIDQAGAILLHNVTETLTLKARNSPDLDRVEDPADSASFPPDLVWTL 180
Qy 181 RDFCLGLEIDQLVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCKCIFDLPA 240
Db 181 RDFCLGLEIDQLVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCKCIFDLPA 240
Qy 241 HQKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
Db 241 HQKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
Qy 301 AISSGDLPCITENAVIALAORENSAAVOKAIYHQOQGVOKVQLPMTETLOELLDLHRTSER 360
Db 301 AISSGDLPCITENAVIALAORENSAAVOKAIYHQOQGVOKVQLPMTETLOELLDLHRTSER 360
Qy 361 EAIEVFMKNSFKVDQSFQKELETLDDAKQNDICKRNLEASSDYCSALLKDI FGPLEEAV 420

Qy 481 TETETKKKKAQVKAERKAEQAORLAALAIQRQNEQMMQERERLHQBQVQVQMEIAKQNWLAEQ 540
Db 481 TETETKKKKAQVKAERKAEQAORLAALAIQRQNEQMMQERERLHQBQVQVQMEIAKQNWLAEQ 540
Qy 541 QKMQEQQM 549
Db 541 QKMQEQQM 549

RESULT 4
US-10-121-049-46
; Sequence 46, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.9e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEIHMSDPMCLLENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
Db 1 MALEIHMSDPMCLLENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
Qy 61 KNGGFSVASTVQSHTKGIWICVPHPNWPNHNTLVLLDTEGLGDVEKADNKNNDIQIFALAL 120
Db 61 KNGGFSVASTVQSHTKGIWICVPHPNWPNHNTLVLLDTEGLGDVEKADNKNNDIQIFALAL 120
Qy 121 LLSTFTYNTVNTKIDQAGAILLHNVTETLTLKARNSPDLDRVEDPADSASFPPDLVWTL 180
Db 121 LLSTFTYNTVNTKIDQAGAILLHNVTETLTLKARNSPDLDRVEDPADSASFPPDLVWTL 180
Qy 181 RDFCLGLEIDQLVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCKCIFDLPA 240
Db 181 RDFCLGLEIDQLVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCKCIFDLPA 240
Qy 241 HQKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
Db 241 HQKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
```

Db 241 HOKKLAQLETPDDELEPEFVQVTEPCSYIFSHSMTKTLPGGIWVNGSRKLNVLVTYN 300
QY 301 AISSGDLPCIEANALAQRENSAAVQKAI AHYDOOMGOKVOLPMETLQELLDLHRTSER 360
Db 301 AISSGDLPCIEANALAQRENSAAVQKAI AHYDOOMGOKVOLPMETLQELLDLHRTSER 360
QY 361 EAIEVFMKNSFKVDQSPQKELETLLDAKNDICRNLEASSDYCSALLKDI FGPLEEAV 420
Db 361 EAIEVFMKNSFKVDQSPQKELETLLDAKNDICRNLEASSDYCSALLKDI FGPLEEAV 420
QY 421 KOGIYKPGGHNLFQKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480
Db 421 KOGIYKPGGHNLFQKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480
QY 481 TTEKKEKAEQVKAERKAEQAORLAAIORQNEOMQERERLHQQVQVQMEIAKQNWLAQ 540
Db 481 TTEKKEKAEQVKAERKAEQAORLAAIORQNEOMQERERLHQQVQVQMEIAKQNWLAQ 540
QY 541 QKMQEQQM 549
Db 541 QKMQEQQM 549

RESULT 5

US-10-123-904-46

; Sequence 46, Application US/10123904

; Publication No. US20030022328A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330R1C54

; CURRENT APPLICATION NUMBER: US/10/123,904

; CURRENT FILING DATE: 2002-04-16

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 46

; LENGTH: 586

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-123-904-46

Query Match 92.5%; Score 2815; DB 14; Length 586;

Best Local Similarity 100.0%; Pred. No. 9.9e-197;

Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEIHSDPMCLIEFNQKVNQEALEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
Db 1 MALEIHSDPMCLIEFNQKVNQEALEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
QY 61 KNGFSVASTVQSHTKGIWICVPHNPHTLVLLDTTEGLDVEKADNKNDIQIFALAL 120
Db 61 KNGFSVASTVQSHTKGIWICVPHNPHTLVLLDTTEGLDVEKADNKNDIQIFALAL 120
QY 121 LLSSTFVNTNKKIDQGAIDLHNVTELTDLKARNSPDLORVEDPADSFFPDLVWTL 180
Db 121 LLSSTFVNTNKKIDQGAIDLHNVTELTDLKARNSPDLORVEDPADSFFPDLVWTL 180

QY 181 RDFCLGLEIDGOLVTPDDEYLENSLRPKQSGDORVQNFNLPRLCIOKFPFKKCFIPDLPA 240
Db 181 RDFCLGLEIDGOLVTPDDEYLENSLRPKQSGDORVQNFNLPRLCIOKFPFKKCFIPDLPA 240
QY 241 HOKKLAQLETPDDELEPEFVQVTEPCSYIFSHSMTKTLPGGIWVNGSRKLNVLVTYN 300
Db 241 HOKKLAQLETPDDELEPEFVQVTEPCSYIFSHSMTKTLPGGIWVNGSRKLNVLVTYN 300
QY 301 AISSGDLPCIEANALAQRENSAAVQKAI AHYDOOMGOKVOLPMETLQELLDLHRTSER 360
Db 301 AISSGDLPCIEANALAQRENSAAVQKAI AHYDOOMGOKVOLPMETLQELLDLHRTSER 360
QY 361 EAIEVFMKNSFKVDQSPQKELETLLDAKNDICRNLEASSDYCSALLKDI FGPLEEAV 420
Db 361 EAIEVFMKNSFKVDQSPQKELETLLDAKNDICRNLEASSDYCSALLKDI FGPLEEAV 420
QY 421 KOGIYKPGGHNLFQKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480
Db 421 KOGIYKPGGHNLFQKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480
QY 481 TTEKKEKAEQVKAERKAEQAORLAAIORQNEOMQERERLHQQVQVQMEIAKQNWLAQ 540
Db 481 TTEKKEKAEQVKAERKAEQAORLAAIORQNEOMQERERLHQQVQVQMEIAKQNWLAQ 540
QY 541 QKMQEQQM 549
Db 541 QKMQEQQM 549

RESULT 6

US-10-140-470-46

; Sequence 46, Application US/10140470

; Publication No. US20030022331A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330R1C160

; CURRENT APPLICATION NUMBER: US/10/140,470

; CURRENT FILING DATE: 2002-05-06

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 46

; LENGTH: 586

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-140-470-46

Query Match 92.5%; Score 2815; DB 14; Length 586;

Best Local Similarity 100.0%; Pred. No. 9.9e-197;

Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEIHSDPMCLIEFNQKVNQEALEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
Db 1 MALEIHSDPMCLIEFNQKVNQEALEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60

Qy 61 KNKGSFVASTVQSHTKGIWICVPHNPWPNHTLVLLDTEGLGDEVEKADNKNNDIQIFALAL 120
Db 61 KNKGSFVASTVQSHTKGIWICVPHNPWPNHTLVLLDTEGLGDEVEKADNKNNDIQIFALAL 120
Qy 121 LLSSTFVYNTVNTKIDQGAIDLHNVNTELTLLKARNSPDLDRVEDPADSASFFPDVWTL 180
Db 121 LLSSTFVYNTVNTKIDQGAIDLHNVNTELTLLKARNSPDLDRVEDPADSASFFPDVWTL 180
Qy 181 RDFCLGLEIDQGLVTPDEYLENSLRPKQSDQORVQNFNLPRLCIQKFPFKKCFIDPLPA 240
Db 181 RDFCLGLEIDQGLVTPDEYLENSLRPKQSDQORVQNFNLPRLCIQKFPFKKCFIDPLPA 240
Qy 241 HOKKLAOLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLTYVN 300
Db 241 HOKKLAOLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLTYVN 300
Qy 301 AISSGDLPCIEAVLALAQRENSAAVQKAI AHYDQMGQKQVQLPMETLQELLDLHRTSER 360
Db 301 AISSGDLPCIEAVLALAQRENSAAVQKAI AHYDQMGQKQVQLPMETLQELLDLHRTSER 360
Qy 361 EAI EVMKNSFKVDVDSQFKELETLDDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420
Db 361 EAI EVMKNSFKVDVDSQFKELETLDDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420
Qy 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVQLKYLSKESVSHAILQTDQAL 480
Db 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVQLKYLSKESVSHAILQTDQAL 480
Qy 481 TETEKKKKEAQVKAEAEKAEQAORLAAIQRONEQMMQERERLHQEVRQMEIAKQNWLAEQ 540
Db 481 TETEKKKKEAQVKAEAEKAEQAORLAAIQRONEQMMQERERLHQEVRQMEIAKQNWLAEQ 540
Qy 541 QKMQEQQMQ 549
Db 541 QKMQEQQMQ 549

RESULT 7
US-10-175-746-46
; Sequence 46, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-46
Query Match 92.5%; Score 2815; DB 14; Length 586;

Best Local Similarity 100.0%; Pred. No. 9.9e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MALEIHNHSDMCLTIENFNEQLKVNQEALEILSALTQPVVVVAIVGLYRTGKSYLMNKLGA 60
Db 1 MALEIHNHSDMCLTIENFNEQLKVNQEALEILSALTQPVVVVAIVGLYRTGKSYLMNKLGA 60
Qy 61 KNKGSFVASTVQSHTKGIWICVPHNPWPNHTLVLLDTEGLGDEVEKADNKNNDIQIFALAL 120
Db 61 KNKGSFVASTVQSHTKGIWICVPHNPWPNHTLVLLDTEGLGDEVEKADNKNNDIQIFALAL 120
Qy 121 LLSSTFVYNTVNTKIDQGAIDLHNVNTELTLLKARNSPDLDRVEDPADSASFFPDVWTL 180
Db 121 LLSSTFVYNTVNTKIDQGAIDLHNVNTELTLLKARNSPDLDRVEDPADSASFFPDVWTL 180
Qy 181 RDFCLGLEIDQGLVTPDEYLENSLRPKQSDQORVQNFNLPRLCIQKFPFKKCFIDPLPA 240
Db 181 RDFCLGLEIDQGLVTPDEYLENSLRPKQSDQORVQNFNLPRLCIQKFPFKKCFIDPLPA 240
Qy 241 HOKKLAOLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLTYVN 300
Db 241 HOKKLAOLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLTYVN 300
Qy 301 AISSGDLPCIEAVLALAQRENSAAVQKAI AHYDQMGQKQVQLPMETLQELLDLHRTSER 360
Db 301 AISSGDLPCIEAVLALAQRENSAAVQKAI AHYDQMGQKQVQLPMETLQELLDLHRTSER 360
Qy 361 EAI EVMKNSFKVDVDSQFKELETLDDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420
Db 361 EAI EVMKNSFKVDVDSQFKELETLDDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420
Qy 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVQLKYLSKESVSHAILQTDQAL 480
Db 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVQLKYLSKESVSHAILQTDQAL 480
Qy 481 TETEKKKKEAQVKAEAEKAEQAORLAAIQRONEQMMQERERLHQEVRQMEIAKQNWLAEQ 540
Db 481 TETEKKKKEAQVKAEAEKAEQAORLAAIQRONEQMMQERERLHQEVRQMEIAKQNWLAEQ 540
Qy 541 QKMQEQQMQ 549
Db 541 QKMQEQQMQ 549

RESULT 8
US-10-176-918-46
; Sequence 46, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550


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; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-46

Query Match      92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.9e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEIHMSDPMCLLENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGSKYLNKLAG 60
Db 1 MALEIHMSDPMCLLENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGSKYLNKLAG 60

QY 61 KNKGSVASTVQSHTKGIWICVPHNPWPNHTLVLLDTEGLGDVEKADKNNDIQIFALAL 120
Db 61 KNKGSVASTVQSHTKGIWICVPHNPWPNHTLVLLDTEGLGDVEKADKNNDIQIFALAL 120

QY 121 LLSSTFVYNTVNTKIDQGAIDLHNVTELTDLKARNSPDLDRVEDPADSASFFPDLVWTL 180
Db 121 LLSSTFVYNTVNTKIDQGAIDLHNVTELTDLKARNSPDLDRVEDPADSASFFPDLVWTL 180

QY 181 RDFCLGLEIDQLVTPDDEYLENSLRPKQSDORVQNFNLPRLCIQKFFPKKCFIDPLA 240
Db 181 RDFCLGLEIDQLVTPDDEYLENSLRPKQSDORVQNFNLPRLCIQKFFPKKCFIDPLA 240

QY 241 HOKKLAQLETPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYN 300
Db 241 HOKKLAQLETPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYN 300

QY 301 AISSGDLPCIEENAVLALAQRENSAAVQKAIHYDQMGQKQVQLPMTTLOELLDLHRTSER 360
Db 301 AISSGDLPCIEENAVLALAQRENSAAVQKAIHYDQMGQKQVQLPMTTLOELLDLHRTSER 360

QY 361 EAIIEVFMKNSPKVDQSFQKELETLLDAKNDICRNLKASDDYCSALLKIDIFGLEEAV 420
Db 361 EAIIEVFMKNSPKVDQSFQKELETLLDAKNDICRNLKASDDYCSALLKIDIFGLEEAV 420

QY 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVQLKYLKSKESVSHAILQTDQAL 480
Db 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVQLKYLKSKESVSHAILQTDQAL 480

QY 481 TETEKKKKEAQVKAEAEKAEQRLAAIORQNEQMMQERERLHQBQVQMEIAKQNWLAEQ 540
Db 481 TETEKKKKEAQVKAEAEKAEQRLAAIORQNEQMMQERERLHQBQVQMEIAKQNWLAEQ 540

QY 541 QKMQEQQMQ 549
Db 541 QKMQEQQMQ 549

RESULT 9
US-10-176-921-46
; Sequence 46, Application US/10176921
; Publication No. US2003002726A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC288
; CURRENT APPLICATION NUMBER: US/10/176,921
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-921-46

Query Match      92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.9e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEIHMSDPMCLLENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGSKYLNKLAG 60
Db 1 MALEIHMSDPMCLLENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGSKYLNKLAG 60

QY 61 KNKGSVASTVQSHTKGIWICVPHNPWPNHTLVLLDTEGLGDVEKADKNNDIQIFALAL 120
Db 61 KNKGSVASTVQSHTKGIWICVPHNPWPNHTLVLLDTEGLGDVEKADKNNDIQIFALAL 120

QY 121 LLSSTFVYNTVNTKIDQGAIDLHNVTELTDLKARNSPDLDRVEDPADSASFFPDLVWTL 180
Db 121 LLSSTFVYNTVNTKIDQGAIDLHNVTELTDLKARNSPDLDRVEDPADSASFFPDLVWTL 180

QY 181 RDFCLGLEIDQLVTPDDEYLENSLRPKQSDORVQNFNLPRLCIQKFFPKKCFIDPLA 240
Db 181 RDFCLGLEIDQLVTPDDEYLENSLRPKQSDORVQNFNLPRLCIQKFFPKKCFIDPLA 240

QY 241 HOKKLAQLETPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYN 300
Db 241 HOKKLAQLETPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYN 300

QY 301 AISSGDLPCIEENAVLALAQRENSAAVQKAIHYDQMGQKQVQLPMTTLOELLDLHRTSER 360
Db 301 AISSGDLPCIEENAVLALAQRENSAAVQKAIHYDQMGQKQVQLPMTTLOELLDLHRTSER 360

QY 361 EAIIEVFMKNSPKVDQSFQKELETLLDAKNDICRNLKASDDYCSALLKIDIFGLEEAV 420
Db 361 EAIIEVFMKNSPKVDQSFQKELETLLDAKNDICRNLKASDDYCSALLKIDIFGLEEAV 420

QY 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVQLKYLKSKESVSHAILQTDQAL 480
Db 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVQLKYLKSKESVSHAILQTDQAL 480

QY 481 TETEKKKKEAQVKAEAEKAEQRLAAIORQNEQMMQERERLHQBQVQMEIAKQNWLAEQ 540
Db 481 TETEKKKKEAQVKAEAEKAEQRLAAIORQNEQMMQERERLHQBQVQMEIAKQNWLAEQ 540

QY 541 QKMQEQQMQ 549
Db 541 QKMQEQQMQ 549

RESULT 10
US-10-137-865-46
; Sequence 46, Application US/10137865
; Publication No. US20030032155A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
```

; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C154
; CURRENT APPLICATION NUMBER: US/10/137,865
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-865-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.9e-197; Indels 0; Gaps 0;
Matches 549; Conservative 0; Mismatches 0;

Qy 1 MALEIHMSDPMCLIEFNEQKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKL 60
Db 1 MALEIHMSDPMCLIEFNEQKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKL 60
Qy 61 KNGFSVASTVQSHTKGIWICVPHNPNTLVLLDTEGLGDVEKADNKNQDIQIFAL 120
Db 61 KNGFSVASTVQSHTKGIWICVPHNPNTLVLLDTEGLGDVEKADNKNQDIQIFAL 120
Qy 121 LLSSTFVNTVNTKIDOGAIDLLHNVTETDLLKARNSPDLDRVEDPADSFFPDVW 180
Db 121 LLSSTFVNTVNTKIDOGAIDLLHNVTETDLLKARNSPDLDRVEDPADSFFPDVW 180
Qy 181 RDFCLGLEIDQLVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFFPKKCFIFDL 240
Db 181 RDFCLGLEIDQLVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFFPKKCFIFDL 240
Qy 241 HOKKLAQLETLDPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVL 300
Db 241 HOKKLAQLETLDPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVL 300
Qy 301 AISSGDLPCIEINAVLALAQRENSAAVOKAIAHYDQMGOKVOLPMETLOELL 360
Db 301 AISSGDLPCIEINAVLALAQRENSAAVOKAIAHYDQMGOKVOLPMETLOELL 360
Qy 361 EAIIEVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKASDDYCSALLKDI 420
Db 361 EAIIEVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKASDDYCSALLKDI 420
Qy 421 KQGIYSKPGGHNLFITQKTEELKAKYRPRKGIQAEVVLQKYLKESVS 480
Db 421 KQGIYSKPGGHNLFITQKTEELKAKYRPRKGIQAEVVLQKYLKESVS 480
Qy 481 TETEKKEAOKVKAEEAKAQAORLAAIORONEQMOERERLHOQVROMETAKQ 540
Db 481 TETEKKEAOKVKAEEAKAQAORLAAIORONEQMOERERLHOQVROMETAKQ 540
Qy 541 QKMQEQQM 549
Db 541 QKMQEQQM 549

RESULT 11

US-10-140-474-46
; Sequence 46, Application US/10140474
; Publication No. US20030032156A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C162
; CURRENT APPLICATION NUMBER: US/10/140,474
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-474-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.9e-197; Indels 0; Gaps 0;
Matches 549; Conservative 0; Mismatches 0;

Qy 1 MALEIHMSDPMCLIEFNEQKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKL 60
Db 1 MALEIHMSDPMCLIEFNEQKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKL 60
Qy 61 KNGFSVASTVQSHTKGIWICVPHNPNTLVLLDTEGLGDVEKADNKNQDIQIFAL 120
Db 61 KNGFSVASTVQSHTKGIWICVPHNPNTLVLLDTEGLGDVEKADNKNQDIQIFAL 120
Qy 121 LLSSTFVNTVNTKIDOGAIDLLHNVTETDLLKARNSPDLDRVEDPADSFFPDVW 180
Db 121 LLSSTFVNTVNTKIDOGAIDLLHNVTETDLLKARNSPDLDRVEDPADSFFPDVW 180
Qy 181 RDFCLGLEIDQLVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFFPKKCFIFDL 240
Db 181 RDFCLGLEIDQLVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFFPKKCFIFDL 240
Qy 241 HOKKLAQLETLDPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVL 300
Db 241 HOKKLAQLETLDPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVL 300
Qy 301 AISSGDLPCIEINAVLALAQRENSAAVOKAIAHYDQMGOKVOLPMETLOELL 360
Db 301 AISSGDLPCIEINAVLALAQRENSAAVOKAIAHYDQMGOKVOLPMETLOELL 360
Qy 361 EAIIEVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKASDDYCSALLKDI 420
Db 361 EAIIEVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKASDDYCSALLKDI 420
Qy 421 KQGIYSKPGGHNLFITQKTEELKAKYRPRKGIQAEVVLQKYLKESVS 480
Db 421 KQGIYSKPGGHNLFITQKTEELKAKYRPRKGIQAEVVLQKYLKESVS 480
Qy 481 TETEKKEAOKVKAEEAKAQAORLAAIORONEQMOERERLHOQVROMETAKQ 540
Db 481 TETEKKEAOKVKAEEAKAQAORLAAIORONEQMOERERLHOQVROMETAKQ 540
Qy 541 QKMQEQQM 549
Db 541 QKMQEQQM 549

RESULT 12

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US-10-142-431-46
; Sequence 46, Application US/10142431
; Publication No. US20030036179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC251
; CURRENT APPLICATION NUMBER: US/10/142,431
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-142-431-46

Query Match      92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.9e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEIHMSDPMCLIEFNEQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60
Db 1 MALEIHMSDPMCLIEFNEQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60

Qy 61 KNKGSVASTVQSHTKGIWICVPHNPNHTLVLLDTEGLDVEKADNKNDIQIFALAL 120
Db 61 KNKGSVASTVQSHTKGIWICVPHNPNHTLVLLDTEGLDVEKADNKNDIQIFALAL 120

Qy 121 LLSSTFVNTVTKIDQGAIDLHNVTETDLKARNSPDLDRVEDPADSASFPDLVMTL 180
Db 121 LLSSTFVNTVTKIDQGAIDLHNVTETDLKARNSPDLDRVEDPADSASFPDLVMTL 180

Qy 181 RDCFLGLEIDGLVTPDEYLENSLRPKQSGDQORVQNFNLPRLCIQKFFPKKCFIFDLPA 240
Db 181 RDCFLGLEIDGLVTPDEYLENSLRPKQSGDQORVQNFNLPRLCIQKFFPKKCFIFDLPA 240

Qy 241 HOKKLAQLETLPPDELEPEFVQVTEPCSYIFSHSMTKTLPGGIMVNGSRLKNLVLYVN 300
Db 241 HOKKLAQLETLPPDELEPEFVQVTEPCSYIFSHSMTKTLPGGIMVNGSRLKNLVLYVN 300

Qy 301 AISSGDLPCIEENAVLALAQRNSAAVQKAIHYDQMGQKQVLPMTLQELLDLHRTSER 360
Db 301 AISSGDLPCIEENAVLALAQRNSAAVQKAIHYDQMGQKQVLPMTLQELLDLHRTSER 360

Qy 361 EAEIVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKNSDYCSALLKDIQFPLEEAV 420
Db 361 EAEIVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKNSDYCSALLKDIQFPLEEAV 420

Qy 481 TETEKKKKAEQVKAERAEKAEQRLAAIQRONEQMMQERLHQBQVQMEIAKQNWLAEQ 540
Db 481 TETEKKKKAEQVKAERAEKAEQRLAAIQRONEQMMQERLHQBQVQMEIAKQNWLAEQ 540
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Qy 541 QKQWQEQQMQ 549
Db 541 QKQWQEQQMQ 549
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RESULT 13

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US-10-143-114-46
; Sequence 46, Application US/10143114
; Publication No. US20030036180A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC211
; CURRENT APPLICATION NUMBER: US/10/143,114
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-143-114-46

Query Match      92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.9e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEIHMSDPMCLIEFNEQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60
Db 1 MALEIHMSDPMCLIEFNEQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60

Qy 61 KNKGSVASTVQSHTKGIWICVPHNPNHTLVLLDTEGLDVEKADNKNDIQIFALAL 120
Db 61 KNKGSVASTVQSHTKGIWICVPHNPNHTLVLLDTEGLDVEKADNKNDIQIFALAL 120

Qy 121 LLSSTFVNTVTKIDQGAIDLHNVTETDLKARNSPDLDRVEDPADSASFPDLVMTL 180
Db 121 LLSSTFVNTVTKIDQGAIDLHNVTETDLKARNSPDLDRVEDPADSASFPDLVMTL 180

Qy 181 RDCFLGLEIDGLVTPDEYLENSLRPKQSGDQORVQNFNLPRLCIQKFFPKKCFIFDLPA 240
Db 181 RDCFLGLEIDGLVTPDEYLENSLRPKQSGDQORVQNFNLPRLCIQKFFPKKCFIFDLPA 240

Qy 241 HOKKLAQLETLPPDELEPEFVQVTEPCSYIFSHSMTKTLPGGIMVNGSRLKNLVLYVN 300
Db 241 HOKKLAQLETLPPDELEPEFVQVTEPCSYIFSHSMTKTLPGGIMVNGSRLKNLVLYVN 300

Qy 301 AISSGDLPCIEENAVLALAQRNSAAVQKAIHYDQMGQKQVLPMTLQELLDLHRTSER 360
Db 301 AISSGDLPCIEENAVLALAQRNSAAVQKAIHYDQMGQKQVLPMTLQELLDLHRTSER 360

Qy 361 EAEIVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKNSDYCSALLKDIQFPLEEAV 420
Db 361 EAEIVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKNSDYCSALLKDIQFPLEEAV 420
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Qy 421 KQIYSKPGGHNLFQKTEELKAKYREPRKGIQAEVQLKYLKESVSHAILQTDQAL 480
Db 421 KQIYSKPGGHNLFQKTEELKAKYREPRKGIQAEVQLKYLKESVSHAILQTDQAL 480
Qy 481 TETEKKEAQQVKAEEAKAEQAORLAAIQRONEQMMQERERLHOFQVROMETAKQNWLAQ 540
Db 481 TETEKKEAQQVKAEEAKAEQAORLAAIQRONEQMMQERERLHOFQVROMETAKQNWLAQ 540
Qy 541 QKMQEQQMQ 549
Db 541 QKMQEQQMQ 549

RESULT 14
US-10-142-419-46
; Sequence 46, Application US/10142419
; Publication No. US20030044945A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C244
; CURRENT APPLICATION NUMBER: US/10/142,419
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-419-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.9e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEIHMSDPMCLINFNQKLVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
Db 1 MALEIHMSDPMCLINFNQKLVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
Qy 61 KNGGFSVASTVQSHTKGIWICVPHNPNTLVLLDTGEGDVEKADNKNDIQIFALAL 120
Db 61 KNGGFSVASTVQSHTKGIWICVPHNPNTLVLLDTGEGDVEKADNKNDIQIFALAL 120
Qy 121 LLSSTFVYNTVYNTKIDQGAIDLHNVTETDLKARNSPDLDRVEDPADSASFFPDVWTL 180
Db 121 LLSSTFVYNTVYNTKIDQGAIDLHNVTETDLKARNSPDLDRVEDPADSASFFPDVWTL 180
Qy 181 RDFCLGLEIDGQVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFPFKKCFIFDLPA 240
Db 181 RDFCLGLEIDGQVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFPFKKCFIFDLPA 240
Qy 241 HOKKLAQLETPDDLEPEFVQVTEFCYIFSHSMTKTLPGGIMVNGSRKLNVLTVYN 300
Db 241 HOKKLAQLETPDDLEPEFVQVTEFCYIFSHSMTKTLPGGIMVNGSRKLNVLTVYN 300
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Db 301 ATSSGDLPCINAVLALAQRNSAAVQKAAIAHYDQMGQKQVQLPMETLQELLDLHRTSER 360
Qy 361 EAIEVFMKNSFKVDQSFQKELETLDDAKQNDICKRNLEASSDYCSALLKDIQFGLPEAV 420
Db 361 EAIEVFMKNSFKVDQSFQKELETLDDAKQNDICKRNLEASSDYCSALLKDIQFGLPEAV 420
Qy 421 KQIYSKPGGHNLFQKTEELKAKYREPRKGIQAEVQLKYLKESVSHAILQTDQAL 480
Db 421 KQIYSKPGGHNLFQKTEELKAKYREPRKGIQAEVQLKYLKESVSHAILQTDQAL 480
Qy 481 TETEKKEAQQVKAEEAKAEQAORLAAIQRONEQMMQERERLHOFQVROMETAKQNWLAQ 540
Db 481 TETEKKEAQQVKAEEAKAEQAORLAAIQRONEQMMQERERLHOFQVROMETAKQNWLAQ 540
Qy 541 QKMQEQQMQ 549
Db 541 QKMQEQQMQ 549

RESULT 15
US-10-123-262-46
; Sequence 46, Application US/10123262
; Publication No. US20030049816A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C38
; CURRENT APPLICATION NUMBER: US/10/123,262
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-262-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.9e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEIHMSDPMCLINFNQKLVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
Db 1 MALEIHMSDPMCLINFNQKLVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
Qy 61 KNGGFSVASTVQSHTKGIWICVPHNPNTLVLLDTGEGDVEKADNKNDIQIFALAL 120
Db 61 KNGGFSVASTVQSHTKGIWICVPHNPNTLVLLDTGEGDVEKADNKNDIQIFALAL 120
Qy 121 LLSSTFVYNTVYNTKIDQGAIDLHNVTETDLKARNSPDLDRVEDPADSASFFPDVWTL 180
Db 121 LLSSTFVYNTVYNTKIDQGAIDLHNVTETDLKARNSPDLDRVEDPADSASFFPDVWTL 180
Qy 181 RDFCLGLEIDGQVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFPFKKCFIFDLPA 240
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Qy	241	HOKKLAQLETLDPDELEPEFVQOVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLYVN	300
Db	241		
Db	241	HOKKLAQLETLDPDELEPEFVQOVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLYVN	300
Qy	301	AISSGDLPCINAVLALAQRENSAAVOKAIAHYDOOMGQKVOLPMETLQELLDLHRTSER	360
Db	301		
Db	301	AISSGDLPCINAVLALAQRENSAAVOKAIAHYDOOMGQKVOLPMETLQELLDLHRTSER	360
Qy	361	EAIEVFMKNSFKDVPDQSFQKELETLLDAKONDI CKRNLEASSDYCSALIKDIFGPLEEAV	420
Db	361		
Db	361	EAIEVFMKNSFKDVPDQSFQKELETLLDAKONDI CKRNLEASSDYCSALIKDIFGPLEEAV	420
Qy	421	KGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL	480
Db	421		
Qy	481	TETEKKEAQAQKAEAKAQAORLAAIORONEQMMQERLHOFVROMETAKONWLAEQ	540
Db	481		
Qy	541	QKMQEQMQ	549
Db	541	QKMQEQMQ	549

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Job time : 164 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2005, 13:15:14 ; Search time 168 Seconds
(without alignments)
1360.568 Million cell updates/sec

Title: US-10-659-549-3
Perfect score: 3043
Sequence: 1 MALETHMSDPMCLIEFNFEQ.....GEARSCSQQQVWSQKVWV 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3043	100.0	591	ADD95076	Human gua
2	2815	92.5	586	AAU12194	Human PRO
3	2815	92.5	586	ABB77445	Human tum
4	2815	92.5	586	ABO17638	Novel hum
5	2815	92.5	586	ABU80892	Human PRO
6	2815	92.5	586	ABU66592	Human PRO
7	2815	92.5	586	ABU59673	Novel sec
8	2815	92.5	586	ABO24863	Human sec
9	2815	92.5	586	ABU66868	Human sec
10	2815	92.5	586	ADA45565	Novel hum
11	2815	92.5	586	ADA75996	Human PRO
12	2815	92.5	586	ADA18646	Human PRO
13	2815	92.5	586	ADA61269	Homo sapi
14	2815	92.5	586	ADB19054	Novel hum
15	2815	92.5	586	ADB27595	Human PRO
16	2815	92.5	586	ADA86074	Novel hum
17	2815	92.5	586	ADA15638	Human PRO
18	2815	92.5	586	ADA47424	Human PRO
19	2815	92.5	586	ADA67219	Human PRO
20	2815	92.5	586	ADB30226	Human PRO
21	2815	92.5	586	ADA85522	Novel hum
22	2815	92.5	586	ADA96734	Human PRO
23	2815	92.5	586	ADA79038	Human PRO
24	2815	92.5	586	ADA87177	Novel hum
25	2815	92.5	586	ADB16379	Human PRO

ALIGNMENTS

RESULT 1

ADD95076

ID ADD95076 standard; protein; 591 AA.

XX AC ADD95076;

XX DT 29-JAN-2004 (first entry)

XX DE Human guanylate binding protein-4 (GBP-4).

XX KW Human; guanylate binding protein-4; GBP-4; myelodysplastic disorder;
myeloproliferative syndrome; acute myeloid leukaemia; cancer; gastric;
lung; colon; melanoma; multiple sclerosis; lung disorder;
intestinal-related disorder; interferon-gamma-induced response;
macrophage; fibroblast; immune cell; neuroprotective; cytostatic.
XX OS Homo sapiens.

Key	Location/Qualifiers
Binding-site	97..100
	/label= GTP-binding consensus motif
	/note= "Specifically claimed in Claim 26"
Modified-site	179..182
	/label= Potential casein_kinase_II_phosphorylation_site
	/note= "Specifically claimed in Claim 26"
Modified-site	179..181
	/label= Potential protein_kinase_C_phosphorylation_site
	/note= "Specifically claimed in Claim 26"
Modified-site	283..288
	/label= Potential N-myristoylation site
	/note= "Specifically claimed in Claim 26"
Modified-site	554..557
	/label= Potential prenylation site
	/note= "Specifically claimed in Claim 26"
Modified-site	562..564
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	/note= "Specifically claimed in Claim 26"
Modified-site	568..571
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	/note= "Specifically claimed in Claim 26"
Modified-site	568..570
	/label= Potential protein_kinase_C_phosphorylation_site
	/note= "Specifically claimed in Claim 26"
Modified-site	579..584
	/label= Potential N-myristoylation site
	/note= "Specifically claimed in Claim 26"
Modified-site	586..588
	/label= Potential protein_kinase_C_phosphorylation_site

26	2815	92.5	586	6	ADA91471	Novel hum
27	2815	92.5	586	6	ADB14534	Human PRO
28	2815	92.5	586	6	ADB18495	Novel hum
29	2815	92.5	586	6	ADA93710	Human PRO
30	2815	92.5	586	6	ADB19606	Novel hum
31	2815	92.5	586	6	ADB12918	Human PRO
32	2815	92.5	586	6	ABO43171	Novel hum
33	2815	92.5	586	6	ADA74172	Human PRO
34	2815	92.5	586	6	ADB24405	Human PRO
35	2815	92.5	586	6	ADA81929	Human PRO
36	2815	92.5	586	6	ADA74892	Human PRO
37	2815	92.5	586	6	ADA84970	Novel hum
38	2815	92.5	586	6	ADA84418	Novel hum
39	2815	92.5	586	6	ADB29674	Human PRO
40	2815	92.5	586	6	ADA80202	Human PRO
41	2815	92.5	586	6	ADA75444	Human PRO
42	2815	92.5	586	6	ADA46669	Human PRO
43	2815	92.5	586	6	ADB24965	Human PRO
44	2815	92.5	586	6	ADA93141	Human PRO
45	2815	92.5	586	6	ADB26491	Human PRO

/note= "Specifically claimed in Claim 26"

FT US6642024-B1.
XX 04-NOV-2003.
PD 17-AUG-2000; 2000US-00643657.
XX 29-JAN-1998; 98US-00015089.
XX (GETH) GENENTECH INC.
PA Pennica D;
XX WPI; 2003-851360/79.
DR N-PSDB; ADD95074, ADD95105.
XX New isolated nucleic encoding guanylate binding protein-4, useful as
PT hybridization probes, in chromosome and gene mapping, treating cancer,
PT e.g. gastric cancer or melanoma or combating immunological and
PT inflammatory responses.
XX Claim 1; SEQ ID NO 3; 60pp; English.
PS The present invention relates to the isolation of a novel human guanylate
CC binding protein (guanylate binding protein-4 or GBP-4), and the
CC polynucleotide sequence encoding it. The polynucleotide sequence encoding
CC GBP-4, the GBP-4 polypeptide, and antibodies to GBP-4 are useful in
CC treating myelodysplastic disorders, myeloproliferative syndromes, acute
CC myeloid leukaemia and cancers (e.g. gastric, lung or colon cancers or
CC melanoma). The polynucleotide sequence is useful as hybridisation probes,
CC in chromosome and gene mapping, in generating transgenic animals, in
CC radioimmunoassays, in inducing formation of anti-GBP-4 antibodies, in
CC combating immunological and inflammatory responses and other pathological
CC conditions (e.g. multiple sclerosis or lung and intestinal-related
CC disorders), as a mediator of any interferon-gamma-induced responses in
CC macrophages and fibroblasts, and may also function in other immune cell
CC populations or in protein processing. The present sequence represents
CC human GBP-4.
XX Sequence 591 AA;
SQ Query Match 100.0%; Score 3043; DB 7; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.1e-241;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALETHMSDPMCLINENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
DB 1 MALETHMSDPMCLINENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
QY 61 KNKGSFVASTVQSHTKGIWICVPHNPNHNTLVLLDTGEGDVEKADKNNDIQIFALAL 120
DB 61 KNKGSFVASTVQSHTKGIWICVPHNPNHNTLVLLDTGEGDVEKADKNNDIQIFALAL 120
QY 121 LLSSTFVYNTVTKIDQGAIDLHNTYETDLKARNSPDLDRVEDPADSAPFPLVWTL 180
DB 121 LLSSTFVYNTVTKIDQGAIDLHNTYETDLKARNSPDLDRVEDPADSAPFPLVWTL 180
QY 181 RDCFLGLEIDGLVTPDEYLENSLRPKQSGDQVQNFNLPRLCIOKFPKCKCFIDPLPA 240
DB 181 RDCFLGLEIDGLVTPDEYLENSLRPKQSGDQVQNFNLPRLCIOKFPKCKCFIDPLPA 240
QY 241 HOKKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLTVYN 300
DB 241 HOKKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLTVYN 300
QY 301 AISSGDLPCJENAVLALAQRENSAAVQKAIHYDQMGQKQVLPMTTQELLDLHRTSER 360
DB 301 AISSGDLPCJENAVLALAQRENSAAVQKAIHYDQMGQKQVLPMTTQELLDLHRTSER 360
QY 361 EAIEVFMKNSFKVDQSFQKLETLDDAKQNDICRNLKREASDDYCSALLKDFGPLEEAV 420
DB 361 EAIEVFMKNSFKVDQSFQKLETLDDAKQNDICRNLKREASDDYCSALLKDFGPLEEAV 420

QY 421 KGIYSKPGHNLFIQKTEELKAKYIYREPRKGIQAEVQLQYKLSKESVSHAILQTDQAL 480
DB 421 KGIYSKPGHNLFIQKTEELKAKYIYREPRKGIQAEVQLQYKLSKESVSHAILQTDQAL 480
QY 481 TETEKKKKEAQVKAEBKAEQAQLAAIQRQNEQMMQBERLHQVQVROMETAKONWLAEQ 540
DB 481 TETEKKKKEAQVKAEBKAEQAQLAAIQRQNEQMMQBERLHQVQVROMETAKONWLAEQ 540
QY 541 QKMQEQQMQVFINCFISPLPVTMEVCSGGEAARSCGSGQGVWSOKVWV 591
DB 541 QKMQEQQMQVFINCFISPLPVTMEVCSGGEAARSCGSGQGVWSOKVWV 591
RESULT 2
AAU12194
ID AAU12194 standard; protein; 586 AA.
XX
AC AAU12194;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO4987 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW eat; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
XX WO200140466-A2.
XX 07-JUN-2001.
XX 01-DEC-2000; 2000WO-US032678.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US000376.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US02031.
PR 23-AUG-2000; 2000WO-US023522.

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OM protein - protein search, using sw model

Run on: July 9, 2005, 13:18:54 ; Search time 172 Seconds
(without alignments)
1759.528 Million cell updates/sec

Title: US-10-659-549-3

Perfect score: 3043

Sequence: 1 MALEIHMDPMCLIFNEQ.....GEARSCGQGVWSQKVVV 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2815	92.5	586	1 GBP5_HUMAN	Q96pp8 homo sapien
2	2516	82.7	489	2 Q86TMS	Q86tm5 homo sapien
3	2490	81.8	504	2 Q8NF03	Q8nf03 homo sapien
4	2236	73.5	481	2 Q8N4O4	Q8n4o4 homo sapien
5	1958.5	64.4	592	1 GBP1_HUMAN	P32455 homo sapien
6	1933	63.5	724	2 Q8BMN7	Q8bm7 mus musculus
7	1907.5	62.7	590	1 GBP5_MOUSE	Q8cfb4 mus musculus
8	1905.5	62.6	561	2 Q8BU78	Q8bu78 mus musculus
9	1897	62.3	591	1 GBP2_HUMAN	P32456 homo sapien
10	1892	62.2	591	2 Q6GPH0	Q6gph0 homo sapien
11	1774.5	58.3	563	2 Q9H0R5	Q9h0r5 homo sapien
12	1765.5	58.0	589	1 GBP1_MOUSE	Q01514 mus musculus
13	1764	58.0	481	2 Q8TCE5	Q8tce5 homo sapien
14	1757.5	57.8	589	1 GBP2_RAT	Q63663 rattus norv
15	1750.5	57.5	589	1 GBP2_MOUSE	Q920e6 mus musculus
16	1528.5	50.2	638	2 Q8N8V2	Q8n8v2 homo sapien
17	1510.5	49.6	633	2 Q6ZN66	Q6zn66 homo sapien
18	1500.5	49.3	640	1 GBP4_HUMAN	Q96pp9 homo sapien
19	1498.5	49.2	640	2 Q6NSL0	Q6nsl0 homo sapien
20	1493.5	49.1	633	2 Q7Z3F0	Q7z3f0 homo sapien
21	1482.5	48.7	638	2 Q8BU48	Q8bu48 mus musculus
22	1482.5	48.7	641	2 Q6KAN1	Q6kan1 mus musculus
23	1479.5	48.6	632	2 Q91Z40	Q91z40 mus musculus
24	1468.5	48.3	620	2 Q8VECS	Q8vec5 mus musculus
25	1459.5	48.0	620	2 Q61107	Q61107 mus musculus
26	1407	46.2	612	2 Q8CFA8	Q8cfa8 mus musculus
27	1392.5	45.8	611	2 Q6ZQL8	Q6zql8 mus musculus
28	1388.5	45.6	447	2 Q9NV33	Q9nv33 homo sapien
29	1377.5	45.3	611	2 Q6PEN2	Q6pen2 mus musculus
30	1365.5	44.9	623	2 Q61594	Q61594 mus musculus
31	1344	44.2	619	2 Q6PG83	Q6pg83 mus musculus

32	1342.5	44.1	595	2 Q6GN80	Q6gn80 xenopus lae
33	1335	43.9	619	2 Q8BTS3	Q8bts3 mus musculus
34	1333	43.8	587	2 Q6DCG7	Q6dgc7 xenopus lae
35	1325.5	43.6	607	2 Q7T0S6	Q7t0s6 xenopus lae
36	1259	41.4	620	2 Q66J21	Q66j21 xenopus lae
37	1229.5	40.4	528	2 Q66IR9	Q66ir9 xenopus lae
38	1198	39.4	635	2 Q6YLY1	Q6yly1 oncorhynch
39	1183	38.9	621	2 Q6DHP7	Q6dhp7 brachydanio
40	1148.5	37.7	385	2 Q8KOG1	Q8kog1 mus musculus
41	1097	36.0	290	2 Q6P3V3	Q6p3v3 homo sapien
42	1054	34.6	576	2 Q90892	Q90892 gallus gall
43	886	29.1	744	2 Q6PCI2	Q6pci2 xenopus lae
44	614.5	20.2	380	2 Q7TMV8	Q7tmv8 mus musculus
45	587.5	19.3	374	2 Q66K09	Q66k09 mus musculus

ALIGNMENTS

RESULT 1
ID GBP5_HUMAN STANDARD; PRT; 586 AA.
AC Q96PP8;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon-induced guanylate-binding protein 5 (GTP-binding protein 5)
DE (Guanine nucleotide-binding protein 5) (GBP-TA antigen)
DE (UNQ2427/PRO4987).
GN Name=GBP5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Avdalovic A., Fu H., Tsurushita N.;
RT "Human GBP-4 and -5: new members of the IFN-gamma-inducible guanylate-binding protein family."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Eichmueller S., Hartmann T., Thiel D., Usener D., Dummer R.,
RT Schadendorf D.;
RL "GBP-TA: a new tumour-specific antigen of cutaneous lymphoma depicted by serological detection."
RN [3]
RP Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
RN [4]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
FAhey J., Helton E., Kettelman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- SIMILARITY: Belongs to the GBP family.
CC -----
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CC -----
DR EMBL; AF288815; AAL02055.1; -;
DR EMBL; AF430642; AAN39035.1; -;
DR EMBL; AF430643; AAN39036.1; -;
DR EMBL; AY358953; AAO93932.1; -;
DR EMBL; BC031639; AAH31639.1; -;
DR HSSP; P32455; 1DG3.
DR Genew; HGNC:19895; GBP5.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02843; GBP; 1.
DR Pfam; PF02841; GBP_C; 1.
KW GTP-binding; Lipoprotein; Multigene family; Prenylation.
FT NP_BIND 45 52 GTP (By similarity).
FT NP_BIND 97 101 GTP (By similarity).
FT LIPID 583 583 S-geranylgeranyl cysteine (By
FT similarity).
SQ SEQUENCE 586 AA; 66617 MW; 95DDC02F0FB705D0 CRC64;

Query Match 92.5%; Score 2815; DB 1; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.7e-134;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALETHMSDPMCLTENFNEQLKVNOEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
DB 1 MALETHMSDPMCLTENFNEQLKVNOEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
QY 61 KNGGFSVASTVQSHTKGIWICVPHPNPNHTLVLLDTGEGLDGVEKADNKNDIQIFALAL 120
DB 61 KNGGFSVASTVQSHTKGIWICVPHPNPNHTLVLLDTGEGLDGVEKADNKNDIQIFALAL 120
QY 121 LLSSTFFVYNTVKNIDQGAIDLHNVNTELTDLKARNSPDLRVEDPADSASFFPDLVWTL 180
DB 121 LLSSTFFVYNTVKNIDQGAIDLHNVNTELTDLKARNSPDLRVEDPADSASFFPDLVWTL 180
QY 181 RDFCLGLEIDGQVTPDDSYLNSLRPKQSGDORVQNFNLPRLCTQKPPKCKCFIDPLPA 240
DB 181 RDFCLGLEIDGQVTPDDSYLNSLRPKQSGDORVQNFNLPRLCTQKPPKCKCFIDPLPA 240
QY 241 HOKKLAQLETPDDLEPEFVQVTEFCYSIFSHSMTKTLPGIWMVNGSRKLNVLTVN 300
DB 241 HOKKLAQLETPDDLEPEFVQVTEFCYSIFSHSMTKTLPGIWMVNGSRKLNVLTVN 300
QY 301 AISSGDLPCIEANVALAQRENSAAVQKAIAYHDQMGQKVLPMETIQELLDLHRTSER 360
DB 301 AISSGDLPCIEANVALAQRENSAAVQKAIAYHDQMGQKVLPMETIQELLDLHRTSER 360
QY 361 EAIKVFKNKSFQVQSQFQKELETLDDAKQNDICRNLKRNLEASDYCSALLKIDFGPLEAV 420
DB 361 EAIKVFKNKSFQVQSQFQKELETLDDAKQNDICRNLKRNLEASDYCSALLKIDFGPLEAV 420

QY 421 KQGIYSKPGGHNFIOQTTELKAKYREPRKGIQAEVLOKYLKSKESVSHAILQTDQAL 480
DB 421 KQGIYSKPGGHNFIOQTTELKAKYREPRKGIQAEVLOKYLKSKESVSHAILQTDQAL 480
QY 481 TETETKKKEAQVKAESAQAORLAATQORNEQMWQERERLHQBQVROMETAKQNWLAEQ 540
DB 481 TETETKKKEAQVKAESAQAORLAATQORNEQMWQERERLHQBQVROMETAKQNWLAEQ 540
QY 541 QKMQEQQMQ 549
DB 541 QKMQEQQMQ 549
RESULT 2
Q86TMS PRELIMINARY; PRT; 489 AA.
ID Q86TMS
AC Q86TMS; 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CTCL tumor antigen GBP-Sta (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Cutaneous lymphoma;
RX PubMed=14996095;
RA Hartmann T.B., Thiel D., Dummer R., Schadendorf D., Eichmuller S.;
RT "SEREX identification of new tumour-associated antigens in cutaneous
RL T-cell lymphoma";
RL Br. J. Dermatol. 150:252-258 (2004).
[2]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Cutaneous lymphoma;
RX PubMed=15175044;
RA Fellenberg F., Hartmann T.B., Dummer R., Usener D., Schadendorf D.,
RA Eichmuller S.;
RT "GBP-5 splicing variants: New guanylate-binding proteins with tumor-
RT associated expression and antigenicity";
RL J. Invest. Dermatol. 122:1510-1517 (2004).
DR EMBL; AF328727; AA040731.1; -;
DR HSSP; P32455; 1DG3.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006935; P:Immune response; IEA.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP; 1.
DR Pfam; PF02841; GBP_C; 1.
FT NON_TER 489 -489
SQ SEQUENCE 489 AA; 55247 MW; B493C3586DFFDAID CRC64;

Query Match 82.7%; Score 2516; DB 2; Length 489;
Best Local Similarity 99.8%; Pred. No. 1.8e-119;
Matches 488; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEIHSMDPMCLTENFNEQLKVNOEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
DB 1 MALEIHSMDPMCLTENFNEQLKVNOEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
QY 61 KNGGFSVASTVQSHTKGIWICVPHPNPNHTLVLLDTGEGLDGVEKADNKNDIQIFALAL 120
DB 61 KNGGFSVASTVQSHTKGIWICVPHPNPNHTLVLLDTGEGLDGVEKADNKNDIQIFALAL 120
QY 121 LLSSTFFVYNTVKNIDQGAIDLHNVNTELTDLKARNSPDLRVEDPADSASFFPDLVWTL 180
DB 121 LLSSTFFVYNTVKNIDQGAIDLHNVNTELTDLKARNSPDLRVEDPADSASFFPDLVWTL 180
QY 181 RDFCLGLEIDGQVTPDDSYLNSLRPKQSGDORVQNFNLPRLCTQKPPKCKCFIDPLPA 240
DB 181 RDFCLGLEIDGQVTPDDSYLNSLRPKQSGDORVQNFNLPRLCTQKPPKCKCFIDPLPA 240

QY 241 HOKKLAQLETLDPDELEPEFVQVTEFCYSIFSHSMTKTLPGGIWNGSRLKLVLTYYN 300
DB 241 HOKKLAQLETLDPDELEPEFVQVTEFCYSIFSHSMTKTLPGGIWNGSRLKLVLTYYN 300
QY 301 AISSGDLPCIEANAVLALAQRENSAAVQKAIHAHYDQMGQKQVLPMTTQELLDLHRTSER 360
DB 301 AISSGDLPCIEANAVLALAQRENSAAVQKAIHAHYDQMGQKQVLPMTTQELLDLHRTSER 360
QY 361 EAEIVFMKNSFKVDVDSFQKELETLLDAKNDICRNLKNSDYCSALLKDIFFGLEEAV 420
DB 361 EAEIVFMKNSFKVDVDSFQKELETLLDAKNDICRNLKNSDYCSALLKDIFFGLEEAV 420
QY 421 KOGIYKPKGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
DB 421 KOGIYKPKGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
QY 481 TETEKKKKE 489
DB 481 TETEKKKKE 489

RESULT 3

Q8NF03 PRELIMINARY; PRT; 504 AA.
AC Q8NF03;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DE FLJ00401 protein (Fragment).
GN Name=FLJ00401;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090479; BAC03460.1; -.
DR HSSP; P32455; 1DG3.
DR GO; GO:000525; F-GTP binding; IEA.
DR GO; GO:0003924; F-GTPase activity; IEA.
DR GO; GO:0006955; P-immune response; IEA.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP; 1.
DR Pfam; PF02841; GBP_C; 1.
FT NON_TER 1
FT NON_TER 504
SQ SEQUENCE 504 AA; 56862 MW; 378814E34539F743 CRC64;

Query Match 81.8%; Score 2490; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 3.9e-118; Mismatches 0; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALEIHSDPMCLIEFNELQKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLANKLAG 60
DB 22 MALEIHSDPMCLIEFNELQKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLANKLAG 81
QY 61 KNGKFSVASTVQSHYKGIWCVPHNPWNTLVLDTGLGDVEKADKNDIQIFALAL 120
DB 82 KNGKFSVASTVQSHYKGIWCVPHNPWNTLVLDTGLGDVEKADKNDIQIFALAL 141
QY 121 LLSSTFVYNTVTKIDQALDILHNVTELTDLKARNSPDLDRVEDPADSFPDLVWTL 180
DB 142 LLSSTFVYNTVTKIDQALDILHNVTELTDLKARNSPDLDRVEDPADSFPDLVWTL 201
QY 181 RDFCLGLEIDGLVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIFDLPA 240
DB 202 RDFCLGLEIDGLVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIFDLPA 261
QY 241 HOKKLAQLETLDPDELEPEFVQVTEFCYSIFSHSMTKTLPGGIWNGSRLKLVLTYYN 300

DB 262 HOKKLAQLETLDPDELEPEFVQVTEFCYSIFSHSMTKTLPGGIWNGSRLKLVLTYYN 321
QY 301 AISSGDLPCIEANAVLALAQRENSAAVQKAIHAHYDQMGQKQVLPMTTQELLDLHRTSER 360
DB 322 AISSGDLPCIEANAVLALAQRENSAAVQKAIHAHYDQMGQKQVLPMTTQELLDLHRTSER 381
QY 361 EAEIVFMKNSFKVDVDSFQKELETLLDAKNDICRNLKNSDYCSALLKDIFFGLEEAV 420
DB 362 EAEIVFMKNSFKVDVDSFQKELETLLDAKNDICRNLKNSDYCSALLKDIFFGLEEAV 441
QY 421 KOGIYKPKGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
DB 442 KOGIYKPKGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 501
QY 481 TET 483
DB 502 TET 504

RESULT 4

Q8N4Q4 PRELIMINARY; PRT; 481 AA.
AC Q8N4Q4;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DE Similar to guanylate binding protein 5 (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033761; AAH33761.1; -.
DR HSSP; P32455; 1DG3.
DR GO; GO:000525; F-GTP binding; IEA.
DR GO; GO:0003924; F-GTPase activity; IEA.
DR GO; GO:0006955; P-immune response; IEA.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP; 1.
DR Pfam; PF02841; GBP_C; 1.
FT NON_TER 1
FT NON_TER 481
SQ SEQUENCE 481 AA; 55070 MW; 3E642C58BCA06895 CRC64;

Query Match 73.5%; Score 2236; DB 2; Length 481;
Best Local Similarity 99.8%; Pred. No. 2.6e-105;
Matches 439; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 110 KNDIQIFALALLSSTFYNTVTKIDQALDILHNVTELTDLKARNSPDLDRVEDPADS 169
DB 5 KNDIQIFALALLSSTFYNTVTKIDQALDILHNVTELTDLKARNSPDLDRVEDPADS 64
QY 170 ASFPDLVWTLRDFCLGLEIDGLVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFP 229
DB 65 ASFPDLVWTLRDFCLGLEIDGLVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFP 124
QY 230 KKKCFIFDLPAHQKLAQLETLDPDELEPEFVQVTEFCYSIFSHSMTKTLPGGIWNGS 289
DB 125 KKKCFIFDLPAHQKLAQLETLDPDELEPEFVQVTEFCYSIFSHSMTKTLPGGIWNGS 184
QY 290 RLKNLVLYVNAISSGDLPCIEANAVLALAQRENSAAVQKAIHAHYDQMGQKQVLPMTTQ 349
DB 185 RLKNLVLYVNAISSGDLPCIEANAVLALAQRENSAAVQKAIHAHYDQMGQKQVLPMTTQ 244
QY 350 ELLDLHRTSREAEIVFMKNSFKVDVDSFQKELETLLDAKNDICRNLKNSDYCSALL 409
DB 245 ELLDLHRTSREAEIVFMKNSFKVDVDSFQKELETLLDAKNDICRNLKNSDYCSALL 304
QY 410 KDIFFGLEEAVKQGIYKPKGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESV 469

Db 305 KDIFGLBEAVKQGIYSKPGHNLFIQKTEELKAKYVPRKGIQAEVLQKYLKSKESV 364
QY 470 SHAILQTOALTEYKTKKKEAQVKAEEAKAEQAQLAAIQRQNEQWQRRERLHQEQVRQM 529
|||||
Db 365 SHAILQTOALTEYKTKKKEAQVKAEEAKAEQAQLAAIQRQNEQWQRRERLHQEQVRQM 424
QY 530 EIAKQNWLAEQKMQEQQM 549
|||||
Db 425 EIAKQNWLAEQKMQEQQM 444
RESULT 5
GBPI HUMAN
ID GBPI HUMAN STANDARD; PRT; 592 AA.
AC P32455;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interferon-induced guanylate-binding protein 1 (GTP-binding protein 1)
DE (Guanine nucleotide-binding protein 1) (HuGBP-1).
GN Name=GBP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91342675; PubMed=1715024;
RA Cheng Y.-S.E., Patterson C.E., Staeheli P.;
RT "Interferon-induced guanylate-binding proteins lack an N(T)KXD
RT consensus motif and bind GMP in addition to GDP and GTP.";
RL Mol. Cell. Biol. 11:4717-4725(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Kainine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kertanan M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP ISOPRENOLID.
RX MEDLINE=96427476; PubMed=8830800;
RA Nantais D.E., Schwemle M., Stickney J.T., Vestal D.J., Buss J.E.;
RT "Prenylation of an interferon-gamma-induced GTP-binding protein: the
RT human guanylate binding protein, HuGBP1.";
RL J. Leukoc. Biol. 60:423-431(1996).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).

RX MEDLINE=20140138; PubMed=10676968; DOI=10.1038/35000617;
RA Prakash B., Praefcke G.J.K., Renault L., Wittigshofer A., Herrmann C.;
RT "Structure of human guanylate-binding protein 1 representing a unique
RT class of GTP-binding proteins.";
RL Nature 403:567-571(2000).
CC -!- FUNCTION: Binds GTP, GDP and GMP.
CC -!- INDUCTION: By interferon gamma during macrophage activation.
CC -!- SIMILARITY: Belongs to the GBP family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M55542; AAA3871.1; -.
DR EMBL; BT006847; AAP35493.1; -.
DR EMBL; BC002666; AAH02666.1; -.
DR PIR; A41268; A41268.
DR PDB; 1DG3; X-ray; A=1-592.
DR PDB; 1FSN; X-ray; A=1-592.
DR Genew; HGNC:4182; GBP1.
DR H-InvDB; HIX0018119; -.
DR MIM; 600411; -.
DR GO; GO:0005525; F:GTP binding; TAS.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP; 1.
DR Pfam; PF02841; GBP_C; 1.
KW 3D-structure; GTP-Binding; Interferon induction; Lipoprotein;
KW Multigene family; Polymorphism; Prenylation.
FT NP_BIND 45 52
FT GTP.
FT NP_BIND 97 101
FT LIPID 589 589
FT VARIANT 349 349
FT S -> T (in dbSNP:1048425).
FT /FTID=VAR_014849.
FT STRAND 11 17
FT TURN 18 19
FT STRAND 20 23
FT HELIX 25 32
FT TURN 33 33
FT STRAND 37 46
FT TURN 47 48
FT HELIX 51 58
FT TURN 59 60
FT STRAND 78 84
FT TURN 89 90
FT STRAND 92 98
FT STRAND 101 101
FT HELIX 104 106
FT TURN 110 111
FT HELIX 112 122
FT STRAND 125 131
FT HELIX 136 140
FT TURN 141 142
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FT STRAND 214 229
FT STRAND 233 237
FT HELIX 244 252
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FT HELIX 260 276
FT STRAND 281 282
FT TURN 283 285

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FT STRAND 286 287
FT STRAND 289 289
FT HELIX 290 306
FT TURN 307 307
FT STRAND 311 311
FT HELIX 312 342
FT HELIX 350 371
FT HELIX 376 378
FT HELIX 379 423
FT TURN 424 427
FT TURN 430 431
FT HELIX 432 449
FT TURN 455 456
FT HELIX 457 467
FT TURN 468 468
FT HELIX 469 478
FT TURN 484 564
FT HELIX 566 592
SQ SEQUENCE 592 AA; 67902 MW; FC05D1B0PB635467 CRC64;

Query Match 64.4%; Score 1958.5; DB 1; Length 592;
Best Local Similarity 69.4%; Pred. No. 3.6e-91;
Matches 387; Conservative 71; Mismatch 89; Indels 11; Gaps 3;

QY 1 MALETHSDPMCLIEFNEOLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLANKLAG 60
DB 1 MASETHMTGPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLANKLAG 60
QY 61 KNGFSVASTVQSHTKGIWICVPHPNWPHHTLVLLDTGGLGDKVEKADNKNDIQIFALAL 120
DB 61 KKGFSLSGTQVSHTKGIWICVPHPNWPHHTLVLLDTGGLGDKVEKADNKNDIQIFALAV 120
QY 121 LLSSTFVYNTVKNIDQGAIDLHNYETLDTLLKARNSPD--LDREVDPADSAPFPDLVW 178
DB 121 LLSSTFVYNSICTINQAMDQLYVVTETLTHIRSKSPDENENEVEDSADPVFPDFFW 180
QY 179 TLRDCLGLEIDQVTPDEYLENSLRPKGSDQVQNFNPLRLCIQKFFPKKCFIDPL 238
DB 181 TLRFSLDLADGQPLTPDEYLYSLKLGKGTGSKDETFNPLRLCIRKFFPKKCFVDFR 240
QY 239 PAHOKKLAQLETLPDDELEPEFVQVTFPCSVIFSHSMTKTLPGGIWNGSLKNLVLT 298
DB 241 PVHRKRLAQLEKQDEELDPEFVQVADFCVIFSNKTKTLUSGGIQQVNGPRLESVLV 300
QY 299 VNAISSGDLPCITENAVLALAQRENSAAVQKALAHYDQMGQKQVQLPMTLQELLDLHRTS 358
DB 301 VNAISSGDLPCMENAVLALAQIENSAAVQKALAHYEQMGQKQVQLPTSLQELLDLHRS 360
QY 359 BREAIEVFWNSFKVDQDSFOKELETLIDAKNDICKNLEASSDYCSALLKIDIFGPLLEE 418
DB 361 BREAIEVTRSSFQVDVHLFQKELAAQLEKKRDFCKQNEASSDRCSGLLQVIFSPLEE 420
QY 419 AVKQGIYKPGGHNLFIQKTELKAKYREPRKGIQAEVQLQYKLSKESVSHALOTDQ 478
DB 421 EVKAGIYKPGGYRFLVQKLDQLKKYEEPRKGIQAEIILQYKLSKESMTDALIQTDQ 480
QY 479 ALTETEKKKAEQVKAERAEKAEARLAAIQRONEQWQERERLHQEVQVQ---MEIAKQ 534
DB 481 TLTEKEKEIEVERVAENASQASAKMLQEMQKNEQMEQKERSYQEHKQLTERKENDRV 540
QY 535 NWLAEEQ-----KMQEEQ 547
DB 541 QLLKEQERTLALKLQEE 558

RESULT 6
Q8BMN7
ID Q8BMN7 PRELIMINARY; PRT; 724 AA.
AC Q8BMN7;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
```

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DE Mus musculus adult male pituitary gland cDNA, RIKEN full-length
DE enriched library, clone:5330409J06 product:weakly similar to GUANYLATE
DE BINDING PROTEIN 5.
DE GN Name=Gbp5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RA The FANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX MEDLINE=20493174; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX MEDLINE=20530913; PubMed=11078661; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX MEDLINE=20530913; PubMed=11078661; DOI=10.1101/gr.152600;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Kato H., Kawai J., Kojima Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK030414; BAC26953.1; -
DR HSSP; P32455; 1DG3.
DR MGD; MGI:2429943; Gbp5.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
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DR GO: 0006955; P: immune response; IEA.
DR InterPro: IPR003191; GBP.
DR Pfam: PF02263; GBP; 1.
DR Pfam: PF02841; GBP_C; 1.
SQ SEQUENCE 724 AA; 80410 MW; 799C517B51DBF47C CRC64;

Query Match 63.5%; Score 1933; DB 2; Length 724;
Best Local Similarity 64.9%; Pred. No. 8.e-90;
Matches 392; Conservative 70; Mismatches 126; Indels 16; Gaps 5;

Qy 1 MALEIHMDDPCLNENFNEQKLVNOEALILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
Dy 1 MAPEIHMDDPCLNENFNEQKLVNOEALILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
Qy 61 KNGKFSVASTVQSHTKGIWICVPHPNPNTLLVLDTEGLGVDKADNKKNDIQIFALAL 120
Dy 61 KNGKFSVASTVQSHTKGIWICVPHPNPNTLLVLDTEGLGVDKADNKKNDIQIFALAI 120
Qy 121 LLSSTFVYNTVNTKIDQGAIDLHNVNTELTDLKARNSPDLDRV--EDPADSASFPDLVW 178
Dy 121 LLSSTFVYNTVNTKIDQGAIDLHNVNTELTDLKARNSPDLDRV--EDPADSASFPDLVW 178
Qy 121 LLSSTFVYNTVNTKIDQGAIDLHNVNTELTDLKARNSPDLDRV--EDPADSASFPDLVW 179
Dy 121 LLSSTFVYNTVNTKIDQGAIDLHNVNTELTDLKARNSPDLDRV--EDPADSASFPDLVW 179
Qy 179 TLRDFCLGLEIDGQAVTDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIPDL 238
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Dy 180 TLRDFCLGLEIDGQAVTDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIPDL 239
Qy 239 PAHOKKLAQLETLDPDELEPEVQVTFEYIFSHSTKTLPGIWMVNGSLKXVLVITY 298
Dy 239 PAHOKKLAQLETLDPDELEPEVQVTFEYIFSHSTKTLPGIWMVNGSLKXVLVITY 298
Qy 240 PALGSKLSQLPSTLSNEELNSDFVQSLSEFCSHIFTSQSKTKLPGGIQVNGPRLSLVITY 299
Dy 240 PALGSKLSQLPSTLSNEELNSDFVQSLSEFCSHIFTSQSKTKLPGGIQVNGPRLSLVITY 299
Qy 299 VNAISSGDLPCENAVLALARENSAAVOKAIAHYDQMGOKVOLPMETLQELDLHRTS 358
Dy 299 VNAISSGDLPCENAVLALARENSAAVOKAIAHYDQMGOKVOLPMETLQELDLHRTS 358
Qy 300 VDANSALPSTIENVTVLARENSAAVOKAIAHYDQMGOKVOLPMETLQELDLHRTS 359
Dy 300 VDANSALPSTIENVTVLARENSAAVOKAIAHYDQMGOKVOLPMETLQELDLHRTS 359
Qy 359 EREAIEVPMKSFQVDSQFQKLETLDAKQNDICRNLKASDYCSALLKDIIFGPLEE 418
Dy 359 EREAIEVPMKSFQVDSQFQKLETLDAKQNDICRNLKASDYCSALLKDIIFGPLEE 418
Qy 360 EREAIEVPMKSFQVDSQFQKLETLDAKQNDICRNLKASDYCSALLKDIIFGPLEE 419
Dy 360 EREAIEVPMKSFQVDSQFQKLETLDAKQNDICRNLKASDYCSALLKDIIFGPLEE 419
Qy 419 AVKQIYKPGGHNLPFQKTELKAKYRPRKQIAQAEVLYOKLYKSEVSHAILQTDQ 478
Dy 419 AVKQIYKPGGHNLPFQKTELKAKYRPRKQIAQAEVLYOKLYKSEVSHAILQTDQ 478
Qy 420 EVAQEFYHKGPGHKLFLQMEQKQKANYRQKQKQAEVLYQVYLNKAKETVSRILQTDQ 479
Dy 420 EVAQEFYHKGPGHKLFLQMEQKQKANYRQKQKQAEVLYQVYLNKAKETVSRILQTDQ 479
Qy 479 ALTEKTEKKKQAEVLYQVYLNKAKETVSRILQTDQ 538
Dy 479 ALTEKTEKKKQAEVLYQVYLNKAKETVSRILQTDQ 538
Qy 480 VLTDKIYKPGGHNLPFQKTELKAKYRPRKQIAQAEVLYOKLYKSEVSHAILQTDQ 539
Dy 480 VLTDKIYKPGGHNLPFQKTELKAKYRPRKQIAQAEVLYOKLYKSEVSHAILQTDQ 539
Qy 539 EQQKMQEQMQ---VFNCIFISPL-----PVTMRVCSGKGEAAARSCGSGQGVWSQ 587
Dy 539 EQQKMQEQMQ---VFNCIFISPL-----PVTMRVCSGKGEAAARSCGSGQGVWSQ 587
Qy 540 EQQKMQEQMQ---VFNCIFISPL-----PVTMRVCSGKGEAAARSCGSGQGVWSQ 597
Dy 540 EQQKMQEQMQ---VFNCIFISPL-----PVTMRVCSGKGEAAARSCGSGQGVWSQ 597
Qy 588 KQWV 591
Dy 588 KQWV 591
Qy 598 ALWI 601
Dy 598 ALWI 601

RESULT 7
GBP5_MOUSE STANDARD; PRT; 590 AA.
AC Q8CFB4; Q8CFB4;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon-induced guanylate-binding protein 5 (GTP-binding protein 5)
DE (Guanine nucleotide-binding protein 5) (MugBP-5).
OS Mus musculus (Mouse).
GN MugBP5
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster;
RC MEDLINE=22284156; PubMed=12396730; DOI=10.1089/107999002760274926;
RX

RA Nguyen T.T., Hu Y., Widney D.P., Mar R.C., Smith J.B.;
RT "Murine GBP-5, a new member of the murine guanylate-binding protein
RT family, is coordinately regulated with other GBPs in vivo and in
RT vitro.";
RL J. Interferon Cytokine Res. 22:899-909 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M., Mural R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=NMRI; TISSUE=Breast tumor;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Fellings E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- SIMILARITY: Belongs to the GBP family.

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or send an email to license@isb-sib.ch).

EMBL: AF422243; AAN31451.1; -
EMBL: AY128412; AAN46362.1; -
EMBL: BC058555; AAN58555.1; -
HSSP: P32455; 1DG3.
MGD: MGI:2429943; Gbp5.
InterPro: IPR003191; GBP.
Pfam: PF02263; GBP; 1.
Pfam: PF02841; GBP_C; 1.
GTP-binding; Lipoprotein; Multigene family; Prenylation.
FT NP_BIND 45 52 GTP (By similarity).
FT NP_BIND 97 101 GTP (By similarity).
FT LIPID 587 587 S-geranylgeranyl cysteine (By
FT similarity).
FT CONFLICT 488 490 KKA -> T (in Ref. 2).
FT CONFLICT 501 501 K -> E (in Ref. 2).
SQ SEQUENCE 590 AA; 66970 MW; 092C0B3F3E0E2D26 CRC64;

Query Match 62.7%; Score 1907.5; DB 1; Length 590;
Best Local Similarity 68.5%; Pred. No. 1.3e-88;
Matches 379; Conservative 62; Mismatches 103; Indels 9; Gaps 3;

Qy 1 MALEIHMDDPCLNENFNEQKLVNOEALILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
Dy 1 MAPEIHMDDPCLNENFNEQKLVNOEALILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
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Dy 61 KNGKFSVASTVQSHTKGIWICVPHPNPNTLLVLDTEGLGVDKADNKKNDIQIFALAI 120
Qy 121 LLSSTFVYNTVNTKIDQGAIDLHNVNTELTDLKARNSPDLDRV--EDPADSASFPDLVW 178
Dy 121 LLSSTFVYNTVNTKIDQGAIDLHNVNTELTDLKARNSPDLDRV--EDPADSASFPDLVW 178


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Db 121 LUSSFTVNTNMKIDQAGAILDLHNVTELDLRTNSSDSNQTGEGPAD-MSFFPDLVW 179
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Db 180 TLRDFCLGLEIDQGLVTPDEYLENSLRPKQSDQVQVNFNLPRLCIQKFFPKKCFIDL 239
Qy 239 PAHQKLAQLETLDPDELEPEFVQVTEFCVSIFSHSMTKTLPGGIMVNGSLKLVLT 298
Db 240 PALGSKLSQPLTSLNEELNSDFVQDSEFCVSIFSHSMTKTLPGGIMVNGSLKLVLT 299
Qy 299 VNAISSGDLPCINAVLALAQRENSAAVQKAIHYDQMGQKQVLPMTQLQELDLHRTS 358
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Qy 359 EREAIEFVKNFSKFDVDSFQKLETLDDAKQNDICRKNLEASSDYCSALLKXDFGPLEE 418
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Qy 419 AVKQIYSKPGGHNFVQKTEBELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQ 478
Db 420 EYAEQFYHKGPGHKLFLQMEQLKANYRQPGKGTQAEVLQKYLKSKESVSHAILQTDQ 479
Qy 479 ALTETEKKKKAEQVKAERAEKAEQVKAERAEKAEQVKAERAEKAEQVKAERAEKAE 533
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Qy 534 -QNWLAEEQKQKOE 545
Db 540 EQWILKQRAQEE 552

RESULT 8
Q8BU78 PRELIMINARY; PRT; 561 AA.
ID Q8BU78
AC Q8BU78
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
DE Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched
DE library, clone:E030025M22 product:weakly similar to GUANYLATE BINDING
DE PROTEIN 5 (Fragment).
GN Name=Gbp5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RW [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RW [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2003).
RW [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RW [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Suno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Nishine T., Harada A.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Iihikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RW [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akimura T., Atakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hasegaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohashi N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK087083; BAC39801.1; --
DR HSP; P32455.1; DG3.
DR MGD; MGI:2429943; Gbp5.
DR GO; GO:000525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; Gbp; 1.
DR Pfam; PF02841; Gbp_C; 1.
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SQ SEQUENCE 561 AA; 63322 MW; 2C83B9838661FF39 CRC64;

Query Match 62.6%; Score 1905.5; DB 2; Length 561;
Best Local Similarity 69.0%; Pred. No. 1.6e-88;
Matches 380; Conservative 60; Mismatches 108; Indels 3; Gaps 2;

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Db 1 MAPEIHMPECLIGSTEGHLVNTQEAUKILSAITQPVVVVAIVGLYRTGKSYLKNKLAG 60
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Db 61 KEKGSFVSTVQSHTKGIWICVPHNPNHTLVLLDTEGLGDKVDEKADNKNDIQIFALAI 120
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Db 121 LLSSTFVYNTVNTKIDQAGAILDLHNVTELDLRTNSSDSNQTGEGPAD-MSFFPDLVW 179
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Qy 239 PAHQKLAQLETLDPDELEPEFVQVTEFCVSIFSHSMTKTLPGGIMVNGSLKLVLT 298
Db 240 PALGSKLSQPLTSLNEELNSDFVQDSEFCVSIFSHSMTKTLPGGIMVNGSLKLVLT 299
Qy 299 VNAISSGDLPCINAVLALAQRENSAAVQKAIHYDQMGQKQVLPMTQLQELDLHRTS 358
Db 300 VDAINSGLPSIENTVVTTLARRENSAAVQKAIHYDQMGQKQVLPMTQLQELDLHRTS 359
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 QY 419 AVKQGIYSKPGHNLFIQKTBELKAKYRPRKGIQAEVLQKYLKSKSVSHAILQTDQ 478
 D 420 EVAQBFYHKPGHKLFLQRMELQKANYRQPGKGTQAEVLTQYLNAKETVSRITLQTDQ 479
 QY 479 ALTETEKKKKAQVKAERAEKAEQRLAIAIQNEQMOERERLHOEQVROMEIAKQNWLA 538
 D 480 VLTDKEIQSKAEQAEARLEAQRLAIAIQNEQMOERERLHOEQVROMEIAKQNWLA 539
 QY 539 EQQKMOEQMQ 549
 D 540 EQQWILKORAQ 550

RESULT 9
 GBP2_HUMAN
 ID GBP2_HUMAN STANDARD; PRT; 591 AA.
 AC P32456; Q86TB0;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interferon-induced guanylate-binding protein 2 (GTP-binding protein 2)
 DE (Guanine nucleotide-binding protein 2) (HUGBP-2).
 GN Name=GBP2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=91342675; PubMed=1715024;
 RP Cheng Y.-S.E., Patterson C.E., Saeheli P.;
 RP "Interferon-induced guanylate-binding proteins lack an N(T)KXD
 RP consensus motif and bind GMP in addition to GDP and GTP.";
 RP Mol. Cell. Biol. 11:4717-4725 (1991).
 RN [2]
 RP REVISIONS.
 RC TISSUE=Foreskin;
 RA Schwemle M.;
 RL Submitted (SEP-1991) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 RA Mewes H.-W., Weil B., Amid C., Fobo G., Han M., Osanger A.,
 RA Wiemann S.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Binds GTP, GDP and GMP.
 CC -!- INDUCTION: By interferon gamma during macrophage activation.
 CC -!- SIMILARITY: Belongs to the GBP family.

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EMBL; M55543; AAA67323.1; -;
 EMBL; AL832451; CAD89925.1; -;
 PIR; S70524; S70524.
 DR HSP; P32455; 1DG3.
 DR Genew; HGNC:4183; GBP2.
 DR H-InvDB; HIX0000764; -;
 DR MIM; 600412; -;
 DR GO; GO:0005525; F:GTP binding; TAS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR InterPro; IPR003191; GBP.
 DR Pfam; PF02263; GBP; 1.

DR Pfam; PF02841; GBP_C; 1.
 KW GTP-binding; Interferon induction; Lipoprotein; Multigene family;
 FT Prenylation. 45 52 GTP (By similarity).
 FT NP_BIND 97 101 GTP (By similarity).
 FT NP_BIND 588 588 S-geranylgeranyl cysteine (By
 FT Lipid similarity).
 FT CONFLICT 303 303 S -> G (in Ref. 3).
 SQ SEQUENCE 591 AA; 67183 MW; E090809EE18FC8A8 CRC64;
 Query Match 62.3%; Score 1897; DB 1; Length 591;
 Best Local Similarity 63.5%; Pred. No. 4.6e-88;
 Matches 377; Conservative 88; Mismatches 101; Indels 28; Gaps 4;
 QY 1 MALEIHMSDPMCLLENFNEOLKVNQALAILSAITQPVVVVAIVGLVYRTGKSYLMNKLQAG 60
 D 1 MAPEINLPGPSLIDNTKQGLVNPPEALKILSAITQPVVVVAIVGLVYRTGKSYLMNKLQAG 60
 QY 61 KNGGFSVASTVQSHTKGIWCVPHNPWPHNHTLVLLDTEGLGDVEKADNKNQDIQIFALAL 120
 D 61 KNGGFSVASTVQSHTKGIWCVPHNPWPHNHTLVLLDTEGLGDVEKADNKNQDIQIFALAL 120
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 D 361 EAEVFMKNSFKVDQSFQKELETLDDAKONDICKRNLEASSDYCSALLKDIQFPLEE 420
 QY 421 KQGIYSKPGHNLFIQKTBELKAKYRPRKGIQAEVLQKYLKSKSVSHAILQTDQ 480
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 D 537 LAEQQ-----KMQEQOQVFINCFISPLPVTMTVCSSGKEGAEAAARSCGSGQGVW 585
 QY 541 MAEQKTLALKLQEQE-----RLKKEGFENESKR---LQKDIW 575
 D 541 MAEQKTLALKLQEQE-----RLKKEGFENESKR---LQKDIW 575

RESULT 10
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 ID Q6GPHO PRELIMINARY; PRT; 591 AA.
 AC Q6GPHO;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Guanylate binding protein 2, interferon-inducible.
 GN Name=GBP2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.R.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.C., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RG Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC073163; AAH73163.1; --
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP; 1.
DR Pfam; PF02841; GBP_C; 1.
SQ SEQUENCE 591 AA; 67233 MW; 739CE562AF335776 CRC64;
Query Match 62.2%; Score 1892; DB 2; Length 591;
Best Local Similarity 63.5%; Pred. No. 8.2e-88;
Matches 377; Conservative 87; Mismatches 102; Indels 28; Gaps 4;
QY 1 MALEIHMSDPMCLIEFNQKLVNOEALILSAITQPVVVAIVGLYRTGSKYLNKLAG 60
DB 1 MAPEINLPQMSLIDNTKQGLVWNPALKILSAITQPVVVAIVGLYRTGSKYLNKLAG 60
QY 61 KNGKFSVASTVQSHTKGIWICVPHNPNTLVLLDTGEGLDVEKADNKNDIQIFALAL 120
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DB 361 EAEIVFMKNSFKVDQSFQKELETLLDAKNDICRNLEASDDYCSALLKIDFGPLEBAV 420
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QY 537 LAEQQ-----KMQEQMQVFINCFISPLPVTMRVCSGKGEAARSCGQGVW 585
DB 541 MAEQEKTALKLQEQE-----RLKKEGFENESKR---LQKDIIW 575
RESULT 11
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AC Q9H0R5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp564C2478.
GN Name=DKFZp564C2478;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RG The German cDNA Consortium;
RA Ottenwälder B., Obermaier B., Deutschenbaur S., Schaiipp A.,
RA Meyes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL136680; CAB6615.1; --
DR HSSP; P32455; IDG3.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP; 1.
DR Pfam; PF02841; GBP_C; 1.
KW Hypothetical protein.
SQ SEQUENCE 563 AA; 64127 MW; 0C2FB7CE7FFCBCC3 CRC64;
Query Match 58.3%; Score 1774.5; DB 2; Length 563;
Best Local Similarity 65.4%; Pred. No. 6.8e-82;
Matches 363; Conservative 61; Mismatches 90; Indels 41; Gaps 3;
QY 1 MALEIHMSDPMCLIEFNQKLVNOEALILSAITQPVVVAIVGLYRTGSKYLNKLAG 60
DB 1 MAPEINLPQMSLIDNTKQGLVWNPALKILSAITQPVVVAIVGLYRTGSKYLNKLAG 60
QY 61 KNGKFSVASTVQSHTKGIWICVPHNPNTLVLLDTGEGLDVEKADNKNDIQIFALAL 120
DB 61 KNGKFSVASTVQSHTKGIWICVPHNPNTLVLLDTGEGLDVEKADNKNDIQIFALAL 120
QY 121 LLSSTFVNTVNTKI DQGAIDLHNVTELTDLKARNSPDLRVEDPADSFFPDVWTL 180
DB 121 LLSSTFVNTVNTKI DQGAIDLHNVTELTDLKARNSPDLRVEDPADSFFPDVWTL 180
QY 181 RDFCLGLIDQLVTPDEYENSLRPKQSGDQVQNFNLPRLCIQKFPKCKCFIDPLA 240
DB 181 RDFSLEADQQLTPDEYENSLRPKQSGDQVQNFNLPRLCIQKFPKCKCFIDPLA 240
QY 241 HQKLAQLETL PDDELEPFVQVTEFCSYIFSHSMTKTLPGGIWNGSRLKNLVITYN 300
DB 241 --RKLAKLEKLODELEPFVQVADFCSYIFSNKTKTLSSGIPVNGPRLESILVITYN 268
QY 301 AISSGDLPCINAVLALAQRENSAAVQKAIHYDQMGQKQVLPMTETLOELLDLHRTSER 360
DB 269 AISRGDLPCMENAVLALAQRENSAAVQKAIHYDQMGQKQVLPMTETLOELLDLHRTSER 328
QY 361 EAEIVFMKNSFKVDQSFQKELETLLDAKNDICRNLEASDDYCSALLKIDFGPLEBAV 420
DB 329 EAEIVFMKNSFKVDHFLFKKLAQLDKRRDFCKQKQAEASDRCSALLQIFSPLEBEV 388
QY 421 KQGYSKPGGHNLFQKTEELKAKYREPRKGIQAEVLQKYLKSKESVSHAIQTQDAL 480
DB 389 KAGIYKPGGVCFLFIQKLDLEKKEYYEPRKGIQAEVLQKYLKSKESVSHAIQTQDAL 448

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